

REMARKS

Applicants submit that the DNA sequence of Pfu DNA polymerase D141A/E143A / V93R mutant (SEQ ID NO: 31) and PFU DNA polymerase D141A/E143A/ V93E mutant (SEQ ID NO: 32) in Figure 13A contain a typographical error between nucleotide positions 1169 and 1171. The corresponding amino acid sequence of Pfu DNA polymerase D141A/E143A / V93R (SEQ ID NO: 44) and PFU DNA polymerase D141A/E143A/ V93E (SEQ ID NO: 46) is shown in Figure 13B as the following sequence ---SYTGG--- (underlining denotes amino acid position 387) which is identical to the amino acid sequence of wild type Pfu DNA polymerase in Figure 20. The presence of Glycine at position 387 is therefore consistent with the sequence GGT between nucleotide positions 1169 and 1171 not the sequence CCN as shown in the originally filed Figure 13A. Hence, the Pfu DNA polymerase D141A/E143A / V93R mutant (SEQ ID NO: 31) and PFU DNA polymerase D141A/E143A/ V93E mutant (SEQ ID NO: 32) sequence in Figure 13A are amended to show the wild type sequence 'GGT' instead of 'CCN' between nucleotide positions 1159 and 1161. No new matter is added.

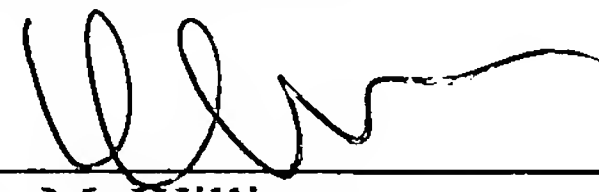
Applicants submit that the DNA sequence encoding Sac7d- Taq fusion protein (SEQ ID NO: 128) in Figure 20 contains typographical errors between nucleotide positions 230 and 232, 343 and 351, and 778 and 780.

Applicants submit that the sequence 'OTC' between positions 142 and 144 within the Taq DNA polymerase sequence and the corresponding amino acid 'X' in Figures 17B, 17C, 17U, 17V, 17NN, 17OO and 17FFF are typographical errors. The wild type DNA sequence at this location is 'GTC' and the corresponding amino acid is Valine as reported in SEQ ID NO:1 of U.S. Patent No. 5,466,591 (Abramson et al., filed February 23 1993) which is incorporated by reference on page 3, line 4 of the present application. Hence the Taq DNA polymerase nucleotide (SEQ ID NO:65) and amino acid (SEQ ID NO: 66) sequences in Figures 17B, 17C, 17U, 17V, 17NN, 17OO and 17FFF are corrected to show the wild type sequence 'GTC' and the corresponding amino acid 'Valine' between positions 142 and 144.

Applicants submit that the amendments of the figures are only made to correct typographical errors and to introduce SEQ ID Nos next to the corresponding nucleotide and amino acid sequences depicted in the Figures and that these amendments do not introduce any new matter.

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Respectfully submitted,



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Amendments to the Drawings:

Applicants further propose amendments to Figures 10, 13 A-B, 14, 17A-17S, 17T-17LL, 17MM-17DDD, 17EEE-17RRR, 18, 19 and 20 herein attached.



FIGURE 10

Figure 10. Oligonucleotide Primers for QuikChange Mutagenesis

V93E#1

5'-gAACATCCCCAAGATgAACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [6]5)

V93E#2

5'-CTTTTCTCTAATAgTgggTTCATCTTggggATgTTC-3' (SEQ ID NO: [7]6)

V93R#1

5'-gAACATCCCCAAGATAgAACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [8]7)

V93R#2

5'-CTTTTCTCTAATAgTgggTCTATCTTggggATgTTC-3' (SEQ ID NO: [9]8)

V93N#1

5'-gAACATCCCCAAGATAAACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [10]9)

V93N#2

5'-CTTTTCTCTAATAgTggggTTATCTTggggATgTTC-3' (SEQ ID NO: [11]10)

V93H#1

5'-gAACATCCCCAAGATCAACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [12]11)

V93H#2

5'-CTTTTCTCTAATAgTggggTgATCTTggggATgTTC-3' (SEQ ID NO: [13]12)

V93X (for saturation mutagenesis; obtained V93G and V93L mutants from library)

5'-(Phosphate)gAACATCCCCAAGATNNKCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [14]13)

V93K#1

5'-gAACATCCCCAAGATAAAACCCACTATTAgAg-3' (SEQ ID NO: [15]14)

V93K#2

5'-CTCTAATAgTgggTTTATCTTggggATgTTC-3' (SEQ ID NO: [16]15)

QCM#1 5'-(Phosphate)gAACATCCCCAAGATgCACCCACTATTAgAgAAAAAg-(SEQ ID NO: [17]16)'

Alanine

QCM#2 5'-(Phosphate)gAACATCCCCAAGATgACCCCACTATTAgAgAAAAAg-3'(SEQ ID NO: [18]17)

Aspartic Acid

Marked-Up Version

QCM#3 5'-(Phosphate)gAACATCCCCAAgATTgCCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [19]18)

Cysteine

QCM#4 5'-

(Phosphate)gAACATCCCCAAgATATACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [20]19)

Isoleucine

QCM#5 5'-(Phosphate)gAACATCCCCAAgATATgCCCACCTATTAgAgAAAAAg-3' (SEQ ID NO: [21]20)

Methionine

QCM#6 5'-(Phosphate)gAACATCCCCAAgATTTCCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [22]21)

Phenylalanine

QCM#7 5'-(Phosphate)gAACATCCCCAAgATCCTCCCACCTATTAgAgAAAAAg-3' (SEQ ID NO: [23]22)

Proline

QCM#8 5'-(Phosphate)gAACATCCCCAAgATAgCCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 23)

Serine

QCM#9 5'-(Phosphate)gAACATCCCCAAgATACACCCCACTATTAgAgAAAAAg- 3' (SEQ ID NO: 24)

Threonine

QCM#10 5'-(Phosphate)gAACATCCCCAAgATTACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 25)

Tyrosine

QCM#11 5'-(Phosphate)gAACATCCCCAAgATTggCCCACCTATTAgAgAAAAAg-3'

(SEQ ID NO: 26)

Tryptophan

MARKED UP VERSION OF AMENDED FIGURE 13A

Please replace Figure 13A with the replacement Figure below, which is marked up by way of bracketing and DOUBLE underlining to show the changes relative to the previous version of Figure 13A.

FIGURE 13A**PFU DNA POLYMERASE**

V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 27)

V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 28)

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ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGAT[XXX]NNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
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GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
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TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
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ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328
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PFU DNA POLYMERASE

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)

V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 29)

V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 30)

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ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGAT[XXX]NNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
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TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAAG AGTGGTTCTT ACTTAGGAAA 1080
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CTCAGGGAGA GCTACACACC NGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
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AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
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GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
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GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

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PFU DNA POLYMERASE

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)

V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 31)

V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 32)

```

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120

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CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGAT[XXX]NNNC CCACTATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
 GGNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
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 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
 AAAAGGGCAG AAAAAGCTTG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTGCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTGAGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
 CTCAGGGAGA GCTACACA[CC N]GGTGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
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 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTGCA 1860
 AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
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 CTCGCAATAT ATGAGCAGAT AACAAAGCCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
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 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

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V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE
 CODONS FOR ARGININE) (SEQ ID NO: 33)

V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ
 ID NO: 34)

ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
 AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
 CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
 ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
 GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGAC[XXX]NNNC CAGCGATAAG GGACAAGATA 300
 CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
 CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
 GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
 AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAATTGGA AGAACGTGGA TCTCCCCTAC 540
 GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
 AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAAC TCGACTTCGC CTATCTGAAA 660
 AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
 ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTGATCTC 780

TATCCTGTGA	TAAGACGGAC	GATAAACCTG	CCCACATACA	CGCTTGAGGC	CGTTTATGAA	840
GCCGTCTTCG	GTCAGCCGAA	GGAGAAGGTT	TACGCTGAGG	AAATAACCAC	AGCCTGGGAA	900
ACCGGCGAGA	ACCTTGAGAG	AGTCGCCCCG	TACTCGATGG	AAGATGCGAA	GGTCACATAC	960
GAGCTTGGGA	AGGAGTTCCT	TCCGATGGAG	GCCCAGCTTT	CTCGCTTAAT	CGGCCAGTCC	1020
CTCTGGGACG	TCTCCCGCTC	CAGCACTGGC	AACCTCGTTG	AGTGGTTCCT	CCTCAGGAAG	1080
GCCTATGAGA	GGAATGAGCT	GGCCCCGAAC	AAGCCCGATG	AAAAGGAGCT	GGCCAGAAGA	1140
CGGCAGAGCT	ATGAAGGAGG	CTATGTAAAA	GAGCCCGAGA	GAGGGTTGTG	GGAGAACATA	1200
GTGTACCTAG	ATTTTAGATC	CCTGTACCCC	TCAATCATCA	TCACCCACAA	CGTCTCGCCG	1260
GATACGCTCA	ACAGAGAAGG	ATGCAAGGAA	TATGACGTTG	CCCCACAGGT	CGGCCACCGC	1320
TTCTGCAAGG	ACTTCCCAGG	ATTTATCCCC	AGCCTGCTTG	GAGACCTCCT	AGAGGAGAGG	1380
CAGAAGATAA	AGAAGAAGAT	GAAGGCCACG	ATTGACCCGA	TCGAGAGGAA	GCTCCTCGAT	1440
TACAGGCAGA	GGGCCATCAA	GATCCTGGCA	AACAGCTACT	ACGGTTACTA	CGGCTATGCA	1500
AGGGCGCGCT	GGTACTGCAA	GGAGTGTGCA	GAGAGCGTAA	CGGCCTGGGG	AAGGGAGTAC	1560
ATAACGATGA	CCATCAAGGA	GATAGAGGAA	AAGTACGGCT	TTAAGGTAAT	CTACAGCGAC	1620
ACCGACGGAT	TTTTTGCCAC	AATACCTGGA	GCCGATGCTG	AAACCGTCAA	AAAGAAGGCT	1680
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GGCTTCTACA	AACGCGGCTT	CTTCGTCACG	AAGAAGAAGT	ATGCGGTGAT	AGACGAGGAA	1800
GGCAAGATAA	CAACGCGCGG	ACTTGAGATT	GTGAGGCGTG	ACTGGAGCGA	GATAGCGAAA	1860
GAGACGCAGG	CGAGGGTTCT	TGAAGCTTTG	CTAAAGGACG	GTGACGTCGA	GAAGGCCGTG	1920
AGGATAGTCA	AAGAAGTTAC	CGAAAAGCTG	AGCAAGTACG	AGGTTCCGCC	GGAGAAGCTG	1980
GTGATCCACG	AGCAGATAAC	GAGGGATTTA	AAGGACTACA	AGGCAACCGG	TCCCCACGTT	2040
GCCGTTGCCA	AGAGGTTGGC	CGCGAGAGGA	GTCAAAATAC	GCCCTGGAAC	GGTGATAAGC	2100
TACATCGTGC	TCAAGGGCTC	TGGGAGGATA	GGCGACAGGG	CGATACCGTT	CGACGAGTTC	2160
GACCCGACGA	AGCACAAGTA	CGACGCCGAG	TACTACATTG	AGAACCAGGT	TCTCCCAGCC	2220
GTTGAGAGAA	TTCTGAGAGC	CTTCGGTTAC	CGCAAGGAAG	ACCTGCGCTA	CCAGAAGACG	2280
AGACAGGTTG	GTTTGAGTGC	TTGGCTGAAG	CCGAAGGGAA	CTTGA	2325	

Vent DNA POLYMERASE

V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 35)

V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 36)

ATGATACTGG	ACACTGATTA	CATAACAAAA	GATGGCAAGC	CTATAATCCG	AATTTTAAAG	60
AAAGAGAACG	GGGAGTTTAA	AATAGAACTT	GACCCTCATT	TTCAGCCCTA	TATATATGCT	120
CTTCTCAAAG	ATGACTCCGC	TATTGAGGAG	ATAAAGGCAA	TAAAGGGCGA	GAGACATGGA	180
AAAACGTGTA	GAGTGCTCGA	TGCAGTGAAA	GTCAGGAAAA	AATTTTGGG	AAGGGAAGTT	240
GAAGTCTGGA	AGCTCATTTT	CGAGCATCCC	CAAGAC [XXX] <u>NNNC</u>	CAGCTATGCG	GGGCAAAATA	300
AGGGAACATC	CAGCTGTGGT	TGACATTTAC	GAATATGACA	TACCCTTTGC	CAAGCGTTAT	360
CTCATAGACA	AGGGCTTGAT	TCCCATGGAG	GGAGACGAGG	AGCTTAAGCT	CCTTGCCTTT	420
GATATTGAAA	CGTTTTATCA	TGAGGGAGAT	GAATTTGGAA	AGGGCGAGAT	AATAATGATT	480
AGTTATGCCG	ATGAAGAAGA	GGCCAGAGTA	ATCACATGGA	AAAATATCGA	TTTGCCGTAT	540
GTCGATGTTG	TGTCCAATGA	AAGAGAAATG	ATAAAGCGTT	TTGTTCAAGT	TGTTAAAGAA	600
AAAGACCCCG	ATGTGATAAT	AAC TTACAAT	GGGGACAATT	TTGATTTGCC	GTATCTCATA	660
AAACGGGCAG	AAAAGCTGGG	AGTTCGGCTT	GTCTTAGGAA	GGGACAAAGA	ACATCCCGAA	720
CCCAAGATTC	AGAGGATGGG	TGATAGTTTT	GCTGTGGAAA	TCAAGGGTAG	AATCCACTTT	780
GATCTTTTCC	CAGTTGTGCG	AAGGACGATA	AACCTCCCAA	CGTATACGCT	TGAGGCAGTT	840
TATGAAGCAG	TTTTAGGAAA	AACC AAAAGC	AAATTAGGAG	CAGAGGAAAT	TGCCGCTATA	900
TGGGAAACAG	AAGAAAGCAT	GAAAAA ACTA	GCCCAGTACT	CAATGGAAGA	TGCTAGGGCA	960
ACGTATGAGC	TCGGGAAGGA	ATTCTTCCCC	ATGGAAGCTG	AGCTGGCAAA	GCTGATAGGT	1020
CAAAGTGAT	GGGACGTCTC	GAGATCAAGC	ACCGGCAACC	TCGTGGAGTG	GTATCTTTTA	1080
AGGGTGGCAT	ACGCGAGGAA	TGAACTTGCA	CCGAACAAAC	CTGATGAGGA	AGAGTATAAA	1140
CGGCGCTTAA	GAACAACTTA	CCTGGGAGGA	TATGTAAAAG	AGCCAGAAAA	AGGTTTGTGG	1200
GAAAAATATCA	TTTATTTGGA	TTTCCGCAGT	CTGTACCCTT	CAATAATAGT	TACTCACAAC	1260
GTATCCCCAG	ATACCCTTGA	AAAAGAGGGC	TGTAAGAATT	ACGATGTTGC	TCCGATAGTA	1320
GGATATAGGT	TCTGCAAGGA	CTTTCGGGGC	TTTATTCCCT	CCATACTCGG	GGA CTTAATT	1380
GCAATGAGGC	AAGATATAAA	GAAGAAAATG	AAATCCACAA	TTGACCCGAT	CGAAAAGAAA	1440
ATGCTCGATT	ATAGGCAAAG	GGCTATTAAA	TTGCTTGCAA	ACAGCTATTA	CGGCTATATG	1500

GGGTATCCTA	AGGCAAGATG	GTACTCGAAG	GAATGTGCTG	AAAGCGTTAC	CGCATGGGGG	1560
AGACACTACA	TAGAGATGAC	GATAAGAGAA	ATAGAGGAAA	AGTTCGGCTT	TAAGGTTCTT	1620
TATGCGGACA	CTGACGGCTT	TTATGCCACA	ATACCCGGGG	AAAAGCCTGA	ACTCATTAAG	1680
AAGAAAGCCA	AGGAATTCCT	AAACTACATA	AACTCCAAAC	TTCCAGGTCT	GCTTGAGCTT	1740
GAGTATGAGG	GCTTTTACTT	GAGAGGATTC	TTTGTTACAA	AAAAGCGCTA	TGCAGTCATA	1800
GATGAAGAGG	GCAGGATAAC	AACAAGGGGC	TTGGAAGTAG	TAAGGAGAGA	TTGGAGTGAG	1860
ATAGCTAAGG	AGACTCAGGC	AAAGGTTTTA	GAGGCTATAC	TTAAAGAGGG	AAGTGTTGAA	1920
AAAGCTGTAG	AAGTTGTTAG	AGATGTTGTA	GAGAAAATAG	CAAAATACAG	GGTTCCTACT	1980
GAAAAGCTTG	TTATCCATGA	GCAGATTACC	AGGGATTTAA	AGGACTACAA	AGCCATTGGC	2040
CCTCATGTCG	CGATAGCAAA	AAGACTTGCC	GCAAGAGGGA	TAAAAGTGAA	ACCGGGCACA	2100
ATAATAAGCT	ATATCGTTCT	CAAAGGGAGC	GGAAAGATAA	GCGATAGGGT	AATTTTACTT	2160
ACAGAATACG	ATCCTAGAAA	ACACAAGTAC	GATCCGGACT	ACTACATAGA	AAACCAAGTT	2220
TTGCCGGCAG	TACTTAGGAT	ACTCGAAGCG	TTTGATACAA	GAAAGGAGGA	TTTAAGGTAT	2280
CAAAGCTCAA	AACAAACCGG	CTTAGATGCA	TGGCTCAAGA	GGTAG		2325

Deep Vent

V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 37)

V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 38)

ATGATACTTG	ACGCTGACTA	CATCACCGAG	GATGGGAAGC	CGATTATAAG	GATTTTCAAG	60
AAAGAAAACG	GCGAGTTTAA	GGTTGAGTAC	GACAGAAACT	TTAGACCTTA	CATTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTCCTGGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCT	CAGGAC[XXX]	<u>NNNC</u>	CCGCAATAAG	GGATAAGATA 300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTTCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAAGG	GACTGGAGAG	AGTTGCAAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAAGTGGAG	GAAAAGTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCCT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220

GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAGTAA 2328

JDF-3

V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE
CODONS FOR ARGININE) (SEQ ID NO: 39)

V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ
ID NO: 40)

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCA
GGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAA
GATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAAGTTCTCGGCAGGTCT
GTGGAGGTCTGGGTCTCTACTTCACGCACCCGAGGAC [XXX] NNNCCGGCAATCCGCGACAAAATAAGGAAGCACCC
CGCGGTTCATCGACATCTACGAGTACGACATACCCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAA
GGTGAGGAAGAGCTTAAACTCATGTCTTCGACATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGGAACCGGGCCGA
TTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGCTGATAACCTGGAAGAAGATCGACCTTCCTTACGTTGAGGT
TGTCTCCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATAC
AACGGCGACAACCTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTTACCCTCGGGAGGGACG
GGAGCGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCC
AGTCATAAGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTTCGGCAAGCCCAAGGAG
AAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCGATGGAGG
ACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCCT
CTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCTCTCTAAGGAAGGCCTACGAGAGGAACGAACTC
GCTCCCAACAAGCCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCTACg_cCGGTGGCTACGTCAAGGAGCCGGAGC
GGGACTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTACCTTCAATCATAATCACCCACAACGTCTCGCC
AGATACGCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCCGAGGTTCGGTCACAAGTTCTGCAAGGACTTCCCC
GGCTTCATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACC
CGCTGGAGAAGAATCTCCTCGATTACAGGCAACGCGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTA
TGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATC
AGAGAGCTTGAGGAAAAGTTTCGGTTTTAAAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGG
ACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACCTGCCCCGGCCTTCTCGAACTCGA
ATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTACGAAGAAAAAGTACGCGGTTCATCGACGAGGAGGGCAAGATAACC
ACGCGCGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGCAGGCGAGGGTTTTGGAGGCGATAC
TCAGGCACGGTGACGTTGAAGAGGCCGTCAGAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCC
GGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCG
AAg_cGTTTGGCCGCCAGAGGTGTTAAATCCGGCCCGGAAGTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGA
TAGGCGACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCA
GGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAG
GTCGGGCTTGGCGCGTGGCTGAAGCCGAAGGGGAAGAAGAAGTGA

MARKED UP VERSION OF AMENDED FIGURE 13B

Please replace Figure 13B with the replacement Figure below, which is marked up by way of bracketing and DOUBLE underlining to show the changes relative to the previous version of Figure 13B.

Figure 13B

>Pfu V93R (SEQ ID NO:41)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVRHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDL PYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRESY
TGGFVKEPEKGLWENIVYLD FRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSL LGHLLERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGL EIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS //

>Pfu V93E (SEQ ID NO:42)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVRHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDL PYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRESY
TGGFVKEPEKGLWENIVYLD FRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSL LGHLLERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGL EIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/G387P (SEQ ID NO:43)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVRHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDL PYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRESY
TPGFVKEPEKGLWENIVYLD FRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSL LGHLLERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGL EIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/D141A/E143A (SEQ ID NO:44)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVRHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDL PYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRESY
TGGFVKEPEKGLWENIVYLD FRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSL LGHLLERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGL EIVRRDW

SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKK

>Pfu V93E/G387P (SEQ ID NO:45)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRESY
TPGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKK

>Pfu V93E/D141A/E143A (SEQ ID NO:46)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKK

>DEEP VENT V93R (SEQ ID NO:47)

MILDADYITEDGKPIIRIFKKENGKFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAOKVRKKFLG
RPIEVWRLYFEHPQDRPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEEAKVITWKKIDLPHYVEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIFHDLYHVIRRTINLPTYTLEAVYEAIIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSTGNLVEWYLLRKAYERNELAPNKPDEREYERRRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFKCDFPGFIPSLKRLDERQ
EIKRKMASKDPIEKMLDYRQRAIKILANSYGYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEFDLRKHKYDAEYYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKK

>DEEP VENT V93E (SEQ ID NO:48)

MILDADYITEDGKPIIRIFKKENGKFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAOKVRKKFLG
RPIEVWRLYFEHPQDEPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEEAKVITWKKIDLPHYVEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIFHDLYHVIRRTINLPTYTLEAVYEAIIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSTGNLVEWYLLRKAYERNELAPNKPDEREYERRRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFKCDFPGFIPSLKRLDERQ
EIKRKMASKDPIEKMLDYRQRAIKILANSYGYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEFDLRKHKYDAEYYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKK

>TGO V93R (SEQ ID NO:49)

MILDTDYITEDGKPVIRIFKKENGFEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDRPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDLPHYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEIEAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLGDLLEERQK
VKKMKATIDPIEKLLDYRQRAIKILANSFYGYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAPERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>TGO V93E (SEQ ID NO:50)

MILDTDYITEDGKPVIRIFKKENGFEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDEPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDLPHYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEIEAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLGDLLEERQK
VKKMKATIDPIEKLLDYRQRAIKILANSFYGYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAPERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>KOD V93R (SEQ ID NO:51)

MILDTDYITEDGKPVIRIFKKENGFEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDRPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPHYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINF
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEIEITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHFRFCKDFPGFIPSLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIEHQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAPERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>KOD V93E (SEQ ID NO:52)

MILDTDYITEDGKPVIRIFKKENGFEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDEPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPHYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINF
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEIEITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHFRFCKDFPGFIPSLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIEHQITRDLKDYKATGPHVAVAKRLAARGVKI

RPGTVISYIVLKSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>VENT V93R (SEQ ID NO:53)

MILDTDYITKDGKPIIRIFKKENGFEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLD AVKVRKKFLG
REVEVWKLIFEHPQDRPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDL PYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRTINLPTYTLEAVYEAVLGKTKSKLGAE EIAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIP SILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIK KKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLV IHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIIISYIVLKSGSGKISDRVILLTEYDPRKHKYDPDYIENQVLP AVLRIEAFGYRKEDLRYQSSKQTGLDA
WLKR

>VENT V93E (SEQ ID NO:54)

MILDTDYITKDGKPIIRIFKKENGFEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLD AVKVRKKFLG
REVEVWKLIFEHPQDEPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDL PYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRTINLPTYTLEAVYEAVLGKTKSKLGAE EIAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIP SILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIK KKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLV IHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIIISYIVLKSGSGKISDRVILLTEYDPRKHKYDPDYIENQVLP AVLRIEAFGYRKEDLRYQSSKQTGLDA
WLKR

>JDF-3 V93R (SEQ ID NO:55)

MILDVDYITENGKPVIRVFKKENGFEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVVKVRAEKVKKKFLGR
SVEVWVLYFTHPQDRPAIRD KIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGTGP
ILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEP KIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAE EIAATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGGYAGGYVK
EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIP SLLGNLLEERQKIKRKM
ATLDPLEKNLLDYRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLV IHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

>JDF-3 V93E (SEQ ID NO:56)

MILDVDYITENGKPVIRVFKKENGFEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVVKVRAEKVKKKFLGR
SVEVWVLYFTHPQDEPAIRD KIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGTGP
ILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEP KIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAE EIAATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGGYAGGYVK
EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIP SLLGNLLEERQKIKRKM
ATLDPLEKNLLDYRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLV IHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

MARKED UP VERSION OF AMENDED FIGURE 14

Please replace Figure 14 with the replacement Figure below, which is marked up by way of bracketing and DOUBLE underlining to show the changes relative to the previous version of Figure 14.

Figure 14

Tgo 93:
NNN = AGA, AGG, CGA, CGC, CGG, CGT (R)
(NUCLEOTIDE SEQUENCE: SEQ ID NO: 57; AMINO ACID SEQUENCE: SEQ ID NO: 58)

NNN = GAA, GAG (E)
(NUCLEOTIDE SEQUENCE: SEQ ID NO: 59; AMINO ACID SEQUENCE: SEQ ID NO: 60)

5'
atg atc ctc gat aca gac tac ata act gag gat gga aag ccc gtc atc 48
Met Ile Leu Asp Thr Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile
1 5 10 15

agg atc ttc aag aag gag aac ggc gag ttc aaa ata gac tac gac aga 96
Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Asp Tyr Asp Arg
20 25 30

aac ttt gag cca tac atc tac gcg ctc ttg aag gac gac tct gcg att 144
Asn Phe Glu Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile
35 40 45

gag gac gtc aag aag ata act gcc gag agg cac ggc act acc gtt agg 192
Glu Asp Val Lys Lys Ile Thr Ala Glu Arg His Gly Thr Thr Val Arg
50 55 60

gtt gtc agg gcc gag aaa gtg aag aag aag ttc cta ggc agg ccg ata 240
Val Val Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Pro Ile
65 70 75 80

gag gtc tgg aag ctc tac ttc act cac ccc cag gac nnn ccc gca atc	288
Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Xaa Pro Ala Ile	
85 90 95	

agg gac aag ata aag gag cat cct gcc gtt gtg gac atc tac gag tac	336
Arg Asp Lys Ile Lys Glu His Pro Ala Val Val Asp Ile Tyr Glu Tyr	
100 105 110	

gac atc ccc ttc gcg aag cgc tac ctc ata gac aaa ggc tta atc ccg	384
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro	
115 120 125	

atg gag ggc gac gag gaa ctt aag atg ctc gcc ttc gac atc gag acg	432
Met Glu Gly Asp Glu Glu Leu Lys Met Leu Ala Phe Asp Ile Glu Thr	
130 135 140	

ctc tat cac gag ggc gag gag ttc gcc gaa ggg cct atc ctg atg ata	480
Leu Tyr His Glu Gly Glu Glu Phe Ala Glu Gly Pro Ile Leu Met Ile	
145 150 155 160	

agc tac gcc gac gag gaa ggg gcg cgc gtt att acc tgg aag aat atc	528
Ser Tyr Ala Asp Glu Glu Gly Ala Arg Val Ile Thr Trp Lys Asn Ile	
165 170 175	

gac ctt ccc tat gtc gac gtc gtt tcc acc gag aag gag atg ata aag	576
Asp Leu Pro Tyr Val Asp Val Val Ser Thr Glu Lys Glu Met Ile Lys	
180 185 190	

cgc ttc ctc aag gtc gtc aag gaa aag gat ccc gac gtc ctc ata acc	624
Arg Phe Leu Lys Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr	
195 200 205	

tac aac ggc gac aac ttc gac ttc gcc tac ctc aag aag cgc tcc gag	672
Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Ser Glu	
210 215 220	

aag ctc gga gtc aag ttc atc ctc gga agg gaa ggg agc gag ccg aaa	720
Lys Leu Gly Val Lys Phe Ile Leu Gly Arg Glu Gly Ser Glu Pro Lys	
225 230 235 240	

atc cag cgc atg ggc gat cgc ttt gcg gtg gag gtc aag gga agg att	768
Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Ile	
245 250 255	

cac ttc gac ctc tac ccc gtc att agg aga acg att aac ctc ccc act	816
His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr	
260 265 270	

tac acc ctt gag gca gta tat gaa gcc atc ttt gga cag ccg aag gag	864
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Gln Pro Lys Glu	
275 280 285	

aag gtc tac gct gag gag ata gcg cag gcc tgg gaa acg ggc gag gga	912
Lys Val Tyr Ala Glu Glu Ile Ala Gln Ala Trp Glu Thr Gly Glu Gly	
290 295 300	

tta gaa agg gtg gcc cgc tac tcg atg gag gac gca aag gta acc tat 960
Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr
305 310 315 320

gaa ctc gga aaa gag ttc ttc cct atg gaa gcc cag ctc tcg cgc ctc 1008
Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
325 330 335

gta ggc cag agc ctc tgg gat gta tct cgc tcg agt acc gga aac ctc 1056
Val Gly Gln Ser Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350

gtc gag tgg ttt ttg ctg agg aag gcc tac gag agg aat gaa ctt gca 1104
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
355 360 365

cca aac aag ccg gac gag agg gag ctg gca aga aga agg gag agc tac 1152
Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Glu Ser Tyr
370 375 380

gcg ggt gga tac gtc aag gag ccc gaa agg gga ctg tgg gag aac atc 1200
Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile
385 390 395 400

gtg tat ctg gac ttc cgc tcc ctg tat cct tcg ata ata atc acc cat 1248
Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His
405 410 415

aac gtc tcc cct gat aca ctc aac agg gag ggt tgt gag gag tac gac	1296
Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Glu Glu Tyr Asp	
420 425 430	

gtg gct cct cag gta ggc cat aag ttc tgc aag gac ttc ccc ggc ttc	1344
Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe	
435 440 445	

atc cca agc ctc ctc gga gac ctc ttg gag gag aga cag aag gta aag	1392
Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys Val Lys	
450 455 460	

aag aag atg aag gcc act ata gac cca atc gag aag aaa ctc ctc gat	1440
Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Lys Lys Leu Leu Asp	
465 470 475 480	

tac agg caa cga gca atc aaa atc ctt gct aat agc ttc tac ggt tac	1488
Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Phe Tyr Gly Tyr	
485 490 495	

tac ggc tat gca aag gcc cgc tgg tac tgc aag gag tgc gcc gag agc	1536
Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser	
500 505 510	

gtt acc gct tgg ggc agg cag tac atc gag acc acg ata agg gaa ata	1584
Val Thr Ala Trp Gly Arg Gln Tyr Ile Glu Thr Thr Ile Arg Glu Ile	
515 520 525	

gag gag aaa ttt ggc ttt aaa gtc ctc tac gcg gac aca gat gga ttt 1632

Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Phe

530

535

540

ttc gca aca ata cct gga gcg gac gcc gaa acc gtc aaa aag aag gca 1680

Phe Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala

545

550

555

560

aag gag ttc ctg gac tac atc aac gcc aaa ctg ccc ggc ctg ctc gaa 1728

Lys Glu Phe Leu Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu Glu

565

570

575

ctc gaa tac gag ggc ttc tac aag cgc ggc ttc ttc gtg acg aag aag 1776

Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys Lys

580

585

590

aag tac gcg gtt ata gac gag gag gac aag ata acg acg cgc ggg ctt 1824

Lys Tyr Ala Val Ile Asp Glu Glu Asp Lys Ile Thr Thr Arg Gly Leu

595

600

605

gaa ata gtt agg cgt gac tgg agc gag ata gcg aag gag acg cag gcg 1872

Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala

610

615

620

agg gtt ctt gag gcg ata cta aag cac ggt gac gtt gaa gaa gcg gta 1920

Arg Val Leu Glu Ala Ile Leu Lys His Gly Asp Val Glu Glu Ala Val

625

630

635

640

Marked-Up Version

agg att gtc aaa gag gtt acg gag aag ctg agc aag tac gag gtt cca 1968

Arg Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro

645

650

655

ccg gag aag ctg gtc atc tac gag cag ata acc cgc gac ctg aag gac 2016

Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile Thr Arg Asp Leu Lys Asp

660

665

670

tac aag gcc acc ggg ccg cat gtg gct gtt gca aaa cgc ctc gcc gca 2064

Tyr Lys Ala Thr Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala

675

680

685

agg ggg ata aaa atc cgg ccc gga acg gtc ata agc tac atc gtg ctc 2112

Arg Gly Ile Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu

690

695

700

aaa ggc tcg gga agg att ggg gac agg gct ata ccc ttt gac gaa ttt 2160

Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe

705

710

715

720

gac ccg gca aag cac aag tac gat gca gaa tac tac atc gag aac cag 2208

Asp Pro Ala Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln

725

730

735

gtt ctt cca gct gtg gag agg att ctg agg gcc ttt ggt tac cgt aaa 2256

Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys

740

745

750

Marked-Up Version

gaa gat tta agg tat cag aaa acg cgg cag gtt ggc ttg ggg gcg tgg 2304

755

cta aaa cct aag aca tga 2322

Figure 17A

Pyrococcus furiosus gene for archaeal histone (Hmf-like) [Fig.17-A]

(ACCESSION No: AB013081)

Nucleotide sequence (SEQ ID NO: 63)

Amino acid sequence (SEQ ID NO: 64)

M	M	G	E	L	P	I	A	P	V	D	R	L	I	R	K	A	G	18
ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
A	Q	R	V	S	E	Q	A	A	K	V	L	A	E	H	L	E	E	36
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
K	A	I	E	I	A	K	K	A	V	D	L	A	K	H	A	G	R	54
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
K	T	V	K	V	E	D	I	K	L	A	I	K	S	*				69
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	TGA				207

Figure 17B

(Hmf-like)-Taq DNA polymerase fusion protein [Fig.17-B]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 64) // Amino acid sequence (SEQ ID NO: 66)

M	M	G	E	L	P	I	A	P	V	D	R	L	I	R	K	A	G	18
ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
A	Q	R	V	S	E	Q	A	A	K	V	L	A	E	H	L	E	E	36
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
K	A	I	E	I	A	K	K	A	V	D	L	A	K	H	A	G	R	54
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
K	T	V	K	V	E	D	I	K	L	A	I	K	S					69
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC					

```

      G   G   G
    // GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   [X]V   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG [O]GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTC GTG GCC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D   L   Y   Q   L   L   S   D   R   I   H   V   L   H   P   E   G   Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G   I   G   E   K   T   A   R   K   L   L   E   E   W   G   S   L   E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

```

A L L K N L L D R L L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC

F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

L A A A R G G R V H R A P E P Y K A
CTG GCC GCC GGC AGG GGC GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CGG GAG GGG GTG GCC CGG CGC TAC GGC

G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

A N L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG

E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GGC AGG CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCG GCC AAG ACC ATC

N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K V R A W I E K T L E E G R R G Y

AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC
V E T L F G R R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCG GCC GCG GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
P K E R A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG
V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG
L S A K E G I D G R G G G H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGA GGC GGC CAT CAT CAT
H H *
CAT CAT TAA

Figure 17C

Taq DNA polymerase- (Hmf-like) fusion protein [Fig.17-C]

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 63)
Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 64)

G G G
// GGC GGC GGT

V T S G M L P L F E P K G R V L L V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTC GTG

D G H H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A [X]V Y G F A K S L L K
AGC CGG GGG GAG CCG GTG CAG GCG [O]GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V F D A K A P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L A R L E V P G Y E A D D V L A S L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L P L E V D F A K R R E P D R E R L

CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
L E S P K A L E E A P W P P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG CCG GAA GGG GCC
F V G G F V L L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
L A A A R G G R V H R A P E P Y K A
CTG GCC GCC GCG AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC CCC ATG CTC CTC GCC
Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CGG GAG GGG GTG GCC CGG CGC TAC GGC
G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
A N L L W G R L E G E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG
E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTC GGC CAC ATG GAG GCC ACG GGG GTG
R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC
S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E K T G K R S T S A A V L E A
GGC AAG ACG AAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC GTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGC GCG GCC AAG ACC ATC

N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K V R A W I E K T L E E G R R G Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

V E T L F G R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCC GCG GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

T A A D L M K L A M V K L L F P R L E
ACC GCC GCC GAC CTC ATG ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

P K E R A E A V -A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCG CGG CTG GCC AAG GAG GTC ATG GAG GGG

V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

L S A K E G I D G R G G G H H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGC CAT CAT CAT CAT

H H //
CAT CAT //

M M G E L P I A P V D R L I R K A G 18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54

A Q R V S E Q A A K V L A E H L E E 36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108

K A I E I A K K A V D L A K H A G R 54
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162

K T V K V E D I K L A I K S * 69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17D

Pfu DNA Polymerase (WT) -(HMF-like) fusion protein [Fig.17-D]

Nucleotide sequence (SEQ ID NO: 61) //Nucleotide sequence (SEQ ID NO: 63)

//
ccctggtcct gggtcacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttcttctct atgagatttt taagtatagt tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaanaatt
taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtctct cggaagcct attaccgtgt ggaaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gtagagaaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaagga gaagagttag gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt ccatattta gcgaaaaggg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga

tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccctga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg gaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaacccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga
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tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaaagac
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gataaaactc ttagcaaatc ctttctacgg atattatggc tatgcaaaaag caagatggta
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gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggctctcta
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tcgtggtta gagatagta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag
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agtaatacaa aagcttgcca attatgaat tccaccagag aagctcgcaa tatatgagca

gataacaaga ccattacatg agtataaggc gataggctct cacgtagctg ttgcaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatat acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggaggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
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tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
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ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaa taccagacga caatgggtgtg ctactcaag ccccatatgg gttgagaaaa


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gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tontcccnga
aagattgaga tgttcttg //
//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

```

Figure 17F

(HMF-like) - Pfu DNA Polymerase (WT) fusion protein [Fig.17-E]

Nucleotide sequence (SEQ ID NO: 63) //Nucleotide sequence (SEQ ID NO: 61)

```

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

ccctggtcct ggggccacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaaccctg gttatagtga caaatcttcc tcaccaccg cccaagaagg ttatttctat
caactctaca cctccccat tttctctctt atgagatttt taagtatatg tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgat tt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt
taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg gaaaaggcat ggaaagattg tgagaattgt
tgatgtagag aagggtgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gtagagaaac atccagcagt

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tgtggacatc ttcgaatag atattccatt tgcaagaga tacctcatcg acaaaggcct
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tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaaagcaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattha gcgaaaaagg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccctga
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ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag
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aggtggattc gttaaagagc cagaaaaagg gtgtgtggaa aacatagtat acctagattt
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aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaat ctttctacgg atatatggc tatgcaaaa caagatggta
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gaaggagctc gaagaaaaagt ttggatttaa agtcctctac attgacactg atggctctcta
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gataacaaga ccattacatg agtataaggc gataggctct cagtagctg ttgcaaaagaa
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ctatctgcat gcttctcttg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga ctctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttctgcgac gtagatcttt
tttgctcaa gcagagccgc tccaatggat aacacccctg ttccgcacc caagtcgcct

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acaatttttt ccttgatatct cctaattgtat aagcaagcca aaggagagta gatgctacct
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aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
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ccagggtaat gttttttaagt atgaaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtag tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatgggtgtg ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtttagc tcntcccnga
aagattgaga tgttcttgg // TGA

```

Figure 17F

(Hmf-like) - pfu DNA POLYMERASE (V93 R OR E) fusion protein [Fig.17-F]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 27)
Nucleotide sequence (SEQ ID NO: 63) //Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT      54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA      108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA      162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

```

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//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240

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ACCGTG TGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGCAG AAAAACTTGG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGA AAGAATTCTT TCCAATGGAA ATTCAAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTA AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGAGTA TCAAAAGAAG 1140
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGTT GTGGGAAAA 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTA CTG CCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTC TCTATGC AACTATCCCA AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAA TTTGTAAAATA CATAAATTCA AAGTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAAATAG TAAAAGAAGT AATACAAAAG CTTGCCAAAT ATGAAATTCC ACCAGAGAA 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAAT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGC AATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAA 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAA AATCC // 2328
// TGA

Figure 17G

PFU DNA POLYMERASE (V93 R OR E) - (HMF-like) fusion protein [Fig.17-G]

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATT TGAACATCCC CAAGATXXXC CCACATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCTTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAAGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGCAG AAAAACTTGG GATTAAATTA ACCATTGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCTTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTA CTGCCCTG GGAAGAAAAG 1560
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GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGA AATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980


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CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
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GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGCATATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

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Figure 17H

PFU DNA POLYMERASE (G387P/V93R OR E) -(HMF-like) fusion protein [Fig.17-H]

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 63)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATT TTGGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTGTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCTC ATATTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCTT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020

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GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTTCT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTA CTGCTG GGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAG 1680
GCTCTAGAAAT TTGTAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGTCTCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTC TTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGCTT AACATTAAA AATCC // 2328

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

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Figure 17I

(Hmf-like) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein [Fig.17-I]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 29)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 30)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATT TTTGAAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTTC 420
GATATAGAAA CCCCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTC AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100

GGATACATAG TACTTAGAG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TAGGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG 2328

Figure 17J

(HMF-LIKE) -PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein
[Fig.17-J]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGGCATGA 180
AAGATTGTA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCG CAAGCCTATT 240
ACCGTGTGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GCNATAGCNA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTAGCG 660
AAAAGGCAG AAAAACTTGG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840

GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAGAAGG 1140
CTCAGGGAGA GCTACACA [CCN]GGT GGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTA CTGCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAA 1980
CTCGCAATAT ATGAGCAGAT AACAAAGCCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAA AATCC // 2328

TGA

Figure 17K

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) - (HMF-LIKE) fusion protein
[Fig.17-K]

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 63)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAATTTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GCNATAGCNA CCTCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCCAAG 720
ATGCAGAGAA TAGCGGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA [CC N] GGTGGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTA CTG CCTG GGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGCGGAT AGTCTCTAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGCATATTCT AGCTGAGGAA 2160

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TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

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Figure 17L

KOD DNA POLYMERASE - (Hmf-like) fusion protein [Fig.17-L]

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 63)

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V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA AGTTCCTCGG GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGACAACCT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTGAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAAG AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
GAGCTTGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGTTGTG GGAGAACATA 1200

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GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GTCCTTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTA CTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGCGG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTGCTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTGCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325
//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
      GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
      AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
      AAG ACC GTT AAG GTC GAA GAC ATT AAG GCA ATT AAG AGC TGA

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Figure 17M

(HMF-like) - KOD DNA POLYMERASE fusion protein [Fig.17-M]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
      GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
      AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
      AAG ACC GTT AAG GTC GAA GAC ATT AAG GCA ATT AAG AGC //

```

//ATGATCCTCG ACACTGACTA CATAACCGAG GATGAAAGC CTGTATAAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAAG AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGAC~~XXC~~ CAGCGATAAG GGACAAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAAGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC CTCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCTGCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTGCA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGTTCCGCC GGAGAAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCACGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17N

(Hmf-like)-Vent DNA POLYMERASE FUSION PROTEIN [Fig.17-N]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT      54
      GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA      108
      AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA      162
      AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //
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ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCCA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCCT CAATAATAGT TACTACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCTT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
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AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAAGCCA AGGAATTCCT AACTACATA AACTCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCTG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTGGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 170

Vent DNA POLYMERASE - (hmf-like) FUSION PROTEIN [Fig.17-O]

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACTGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAA 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCCTCATT TTCAGCCCTA TATATAGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAA AATTTTGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGC AAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGCCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTGGAA AGGCGGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GCCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAAAT TTGATTGGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGCACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960

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ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAAC TTA CCTGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAATATATCA TTTATTTTGA TTTCCGCAGT CTGTACCCCT CAATAATAGT TACTACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAA TTGACCCGAT CGAAAAAGAAA 1440
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCT CCATACCTCG GACTTAATT 1380
GCAATGAGGC AAGATATAA AAGAAAAATG AATCCACAA TTGACCCGAT CGAAAAAGAAA 1440
ATGCTCGATT ATAGGCAAG GGCATTATAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAAGCCA AGGAATTCCT AAAC TACATA AACTCCAAC TTCCAGGCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTAA GAGGCTATAC TTAAAGAGGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTG CGATAGCAAA AAGACTTGCC GCAAGAGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGAGATA GCGATAGGT AATTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTGGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //
```

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17P

Deep Vent- (Hmf-like) DNA polymerase fusion protein [Fig.17-P]

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATACTTG ACGCTGACTA CATCACCAGG GATGGGAAGC CGATTATAAG GATTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTACGCT 120

CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTCCTGGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCCT	CAGGACXXXC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTTCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGCCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGGAAGA	AGCCAAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCCTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAAGG	GACTGGAGAG	AGTTGCAAAG	TATTCAATGG	AGGATGCAAA	GGTAAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AAC TTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAAG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGAGGGGAA	1560
TATATAGAGT	TCGTAAAGGAA	GAAACTGGAG	GAAAAGTTCTG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGCCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG	TTAAGGAGGT	AAC TGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG //		2328

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT

GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA

AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA

54108162

AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17Q

(Hmfllike) - Deep Vent DNA polymerase fusion protein [Fig.17-Q]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

//ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC 360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCCTAC 540
GTCGAGGTAG TTTCCAGCGA GAGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG ATGTTATAAT TACCTACAAC GCGGATTCTT TCGACCTTCC CTATCTAGTT 660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG 900
ACTGGAAGG GACTGGAGAG AGTTGCAAG TATTCAATGG AGGATGCAAA GGTAACGTAC 960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAAGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC 1320

AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GAAACTGGAG	GAAAAGTTCC	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGAGTAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17R

JDF-3 - (Hmf-like) fusion protein [Fig.17-R]

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT
ACGGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGGAGAGAGTGAAGAAAAGTTCCCTCGG
CAGGTCTGTGAGGTCGTGGTCCCTACTTCACGCACCCCGCAGGACXXXCCGCAATCCCGACAAAATAAGGAAGCACCCCGGTCATCGACATCTACGAGTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAAGGGCCTAATCCGATGGAAAGGTGAGGAAGAGCTTAAACTCATGTCTTCGACATCGACGCTCTACCCGAGGAGAAAGAGTTTGGAA
CCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGGTGATAACCTGGAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGAAAGGAGATGATTAA
GCGCTTCTTGAGGTCGTTAAGGAGAAAGGACCCGGACGCTGTGATAACATACACGGCGACAACCTTCGACTTCGCCCTACCTGAAAAGCGCTGTGAGAAAGCTTGGCGTGAGCTTT
ACCTTCGGGAGGACGGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTGGCGTCGAGGTGAAGGGCAGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAA
ACCTCCCGACCTACACCCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAAGTCTACGCCGAGGAGATAGCCACCGCTGGAGACCGGGGCTTGAGAG
GGTCGGCGCTACTCGATGGAGGACGGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCGATGGAGGCCCAGCTTTCAGGCTCATCGGCCAAGCCTCTGGGACGTTTCC
CGCTCCAGCACCGGCAACCTCGTCGAGTGTTCCCTCCTAAGGAAGCCCTACGAGAGGAACGAACCTCGCTCCCAACAGCCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGGCT
ACGcCGGTGGCTACGTCAAGGAGCCGGAGCGGGACTGTGGACAATATCGTGATCTAGACTTTCGTAGTCTCTACCTTCAATCATATAATCACCCACAACGTCCTCGCCAGATAC
GCTCAACCGGAGGGGTGTAGGAGCTACGACGTTGCCCGGAGGTCGCTCACAAGTTCTGCAAGGACTTCCCCGGCTTCATTCGGAGCCCTGCTCGGAAACCTGCTGGAGGAAAGG

CAGAAGATAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAAATCTCCTCGATTACAGGCAACGCGCCATCAAGATTTCTCGCCAACAGCTACTACGGCTACTACGGCT
ATGCCAGGGCAAGATGGTACTGCAAGGAGTGCGCCGAGAGCGTTACGGCATGGGAAGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAGTTTCGGTTTTTAAAGTCCT
CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTTAAACTATATCAATCCCAACTGCCCGCCTTCTC
GAACTCGAATACGAGGGCTTCTACGTACGAGGGCTTCTTCGTACGAAAGAAAAAGTACGCGGTCAATCGACGAGGAGGCAAGATAACCAACGCGGGCTTGAGATAGTCAGGCGCG
ACTGGAGCGAGATAGCGAAGGAGACGCGAGGGTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCCGTCAGAAATTGTCAGGGAAGTCAACGAAAGCTGAGCAA
GTACGAGGTTCCGCCGGAAGCTGGTTATCCACGAGCAGATAAACGCGGAGCTCAAGGACTACAAGGCCACCGGCCCGACGTAGCCATAGCGAAGcGTTTGGCCGCCAGAGGT
GTTAAATCCGGCCCCGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGCGCACAGGGCGATTCCCTTCGACGAGTTTCGACCCGACGAAAGCACAAAGTACGATG
CGGACTACTACATCGAACCAGGTTCTGCGCGCAGTTGAGAGAAATCCTCAGGGCCTTCGGCTACCCGCAAGGAAGACCTGCGCTACCAAGAGACGAGGAGGTCTGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAG//

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17S

(Hmf-like) - JDF-3 fusion protein [Fig.17-S]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGTCCTTCAAGAAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGGAGTTCGAG
CCCTACTTCTACGCGTCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGGAGAGGCACGGCAGGTCGTTAAGGTTAAGCGCGCGGAGAAGGT
GAAGAAAGTTCCCTCGCAGGTCGTGTGAGGTCGTGGTCTCTACTTCAACGACCCGACGACXXXCCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGTCA
TCGACATCTACGAGTACGACATACCCCTTCGCCAAGCGCTACCTCATAGACAAGGCCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTCGATC
GAGACGCTCTACCAAGGAGAGAGATTGGAACCGGGCCGATTCTGATGATAAGCTACGCCGATGAAGCGAGGCGCGCTGATAACCTGGAAGAAGATCGACCT
TCCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAGCGCTTCTTGAGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATACAACGGCGACAACCT
TCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAAGCTTGGCGTGAGCTTTACCCTCGGAGGGACGGAGCCGGAAGATACAGCGCATGGGGACAGGTTTGCG
GTCGAGGTGAAGGCGAGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCGACCTACACCTTGAGGCTGTATACGAGCGGTTTTCGGCAA
GCCCCAAGGAGAAAGGTCACGCCGAGGAGATAGCCACCGCCTGGGAGACCGCGAGGGCTTGAGAGGGTCGCGGCTACTCGATGGAGGACCGGAGGGTTACCTACG

AGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCCAGCTTTCAGGCTCATCGGCCAAGGCCCTCTGGACGTTTCCCGCTCCAGCACCCGGCAACCTCGTCGAGTGGTTC
CTCCTAAGGAAGGCCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGGGCTACgcCGGTGGCTACGTCAAGGAGCCC
GGAGCGGGACTGTGGGACAAATATCGTGTAATCTAGACTTTCGTAGTCTCTAqCCTTCAATCATAATCACCCACAACGTCTCGCCAGATACGCTCAACCGCGAGGGGT
GTAGGAGCTACGACGTTGCCCCCGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCCGGCTTCATTCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAAGATA
AAGAGGAAGATGAAGGCAACTCTCGACCCCGCTGGAGAAGAAATCTCCTCGATTACAGGCCAACGqGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTA
TGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAGTTTCGGTTTTA
AAGTCCCTATGCAGACACAGACGGTCTCCATGCCACCAATTCCTGGAGCGGACGCTGAACAGTCAAGAAAGGCAATGGAGTTCTTAAACTATATCAATCCCCAAA
CTGCCCCGGCCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTCGTCACGAAGAAAAGTACGCGGTCAATCGACGAGGCGCAAGATAACCCACGCG
CGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGACGCGAGGGTTTGGAGGCCGATACTCAGGCACGGTGACGTTGAAGAGGCCCGTCAGAA
TTGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCCCGAGCTCAAGGACTACAAGGCCACCGGC
CCGCACGTAGCCATAGCGAAgcGTTTGGCCGCCAGAGGTGTTAAATCCGGCCCGGAACCTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGGAAGGATAGGCGACAG
GGCGATTCCCCTTCGACGAGTTCGACCCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCCCGCAAGTTGAGAGAAATCCTCAGGGCCTTCG
GCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGCGTGGCTGA

Figure 17T

Pyrococcus furiosus DSM 3638, Archaeal hostone (HMf-1) section 85 of 173 of the complete genome.
ACCESSION No: AE010210 REGION: complement (8333..9082) [Fig.17-T]
/product="pcna sliding clamp (proliferating-cell nuclear antigen) "

Nucleotide sequence (SEQ ID NO: 67)

Amino acid sequence (SEQ ID NO: 68)

M	P	F	E	I	V	F	E	G	A	K	E	F	A	Q	L	I	D	18
ATG	CCA	TTT	GAA	ATC	GTA	TTT	GAA	GGT	GCA	AAA	GAG	TTT	GCC	CAA	CTT	ATA	GAC	54
T	A	S	K	L	I	D	E	A	A	F	K	V	T	E	D	G	I	36
ACC	GCA	AGT	AAG	TTA	ATA	GAT	GAG	GCC	GCG	TTT	AAA	GTT	ACA	GAA	GAT	GGG	ATA	108
S	M	R	A	M	D	P	S	R	V	V	L	I	D	L	N	L	P	54
AGC	ATG	AGG	GCC	ATG	GAT	CCA	AGT	AGA	GTT	GTC	CTG	ATT	GAC	CTA	AAT	CTC	CCG	162
S	S	I	F	S	K	Y	E	V	V	E	P	E	T	I	G	V	N	72
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC		216
M	D	H	L	K	K	I	L	K	R	G	K	A	K	D	T	L	I	90
ATG	GAC	CAC	CTA	AAG	AAG	ATC	CTA	AAG	AGA	GGT	AAA	GCA	AAG	GAC	ACC	TTA	ATA	270
L	K	K	G	E	E	N	F	L	E	I	T	I	Q	G	T	A	T	108
CTC	AAG	AAA	GGA	GAG	GAA	AAC	TTC	TTA	GAG	ATA	ACA	ATT	CAA	GGA	ACT	GCA	ACA	324
R	T	F	R	V	P	L	I	D	V	E	E	M	E	V	D	L	P	126
AGA	ACA	TTT	AGA	GTT	CCC	CTA	ATA	GAT	GTA	GAA	GAG	ATG	GAA	GTT	GAC	CTC	CCA	378
E	L	P	F	T	A	K	V	V	V	L	G	E	V	L	K	D	A	144
GAA	CTT	CCA	TTC	ACT	GCA	AAG	GTT	GTA	GTT	CTT	GGA	GAA	GTC	CTA	AAA	GAT	GCT	432
V	K	D	A	S	L	V	S	D	S	I	K	F	I	A	R	E	N	162
GTT	AAA	GAT	GCC	TCT	CTA	GTG	AGT	GAC	AGC	ATA	AAA	TTT	ATT	GCC	AGG	GAA	AAT	486

E	F	I	M	K	A	E	G	E	T	Q	E	V	E	I	K	L	T	180
GAA	TTT	ATA	ATG	AAG	GCA	GAG	GGA	GAA	ACC	CAG	GAA	GTT	GAG	ATA	AAG	CTA	ACT	540
L	E	D	E	G	L	L	D	I	E	V	Q	E	E	T	K	S	A	198
CTT	GAA	GAT	GAG	GGA	TTA	TTG	GAC	ATC	GAG	GTT	CAA	GAG	GAG	ACA	AAG	AGC	GCA	594
Y	G	V	S	Y	L	S	D	M	V	K	G	L	G	K	A	D	E	216
TAT	GGA	GTC	AGC	TAT	CTC	TCC	GAC	ATG	GTT	AAA	GGA	CTT	GGA	AAG	GCC	GAT	GAA	648
V	T	I	K	F	G	N	E	M	P	M	Q	M	E	Y	Y	I	R	234
GTT	ACA	ATA	AAG	TTT	GGA	AAT	GAA	ATG	CCC	ATG	CAA	ATG	GAG	TAT	TAC	ATT	AGA	702
D	E	G	R	L	T	F	L	L	A	P	R	V	E	E	*			250
GAT	GAA	GGA	AGA	CTT	ACA	TTC	CTA	CTG	GCT	CCA	AGA	GTT	GAA	GAG	TGA			750

Figure 17U

(PCNA)-Taq DNA polymerase fusion protein [Fig.17-U]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 68) // Amino acid sequence (SEQ ID NO: 66)

M	P	F	E	I	V	F	E	G	A	K	E	F	A	Q	L	I	D	18
ATG	CCA	TTT	GAA	ATC	GTA	TTT	GAA	GGT	GCA	AAA	GAG	TTT	GCC	CAA	CTT	ATA	GAC	54
T	A	S	K	L	I	D	E	A	A	F	K	V	T	E	D	G	I	36
ACC	GCA	AGT	AAG	TTA	ATA	GAT	GAG	GCC	GCG	TTT	AAA	GTT	ACA	GAA	GAT	GGG	ATA	108
S	M	R	A	M	D	P	S	R	V	V	L	I	D	L	N	L	P	54
AGC	ATG	AGG	GCC	ATG	GAT	CCA	AGT	AGA	GTT	GTC	CTG	ATT	GAC	CTA	AAT	CTC	CCG	162
S	S	I	F	S	K	Y	E	V	V	E	P	E	T	I	G	V	N	72
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC	216
M	D	H	L	K	K	I	L	K	R	G	K	A	K	D	T	L	I	90

ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270

L K K G E E N F L E I T I Q G T A T 108

CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324

R T F R V P L I D V E E M E V D L P 126

AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378

E L P F T A K V V V L G E V L K D A 144

GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432

V K D A S L V S D S I K F I A R E N 162

GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486

E F I M K A E G E T Q E V E I K L T 180

GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540

L E D E G L L D I E V Q E E T K S A 198

CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594

Y G V S Y L S D M V K G L G K A D E 216

TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648

V T I K F G N E M P M Q M E Y Y I R 234

GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702

D E G R L T F L L A P R V E E 250

GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG

G G G

// GGC GGC GGT

V T S G M L P L F E P K G R V L L V

GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D G H H L A Y R T F H A L K G L T T

GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A [X]V Y G F A K S L L K
AGC CGG GGG GAG CCG GTG CAG GCG [O]GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V V F D A K A P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
TCC TTC CGC CAC GAG GCG TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L A R L E V P G Y E A D D V L A S L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L P L E V D F A K R R R E P D R E R L

CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG CCG GAA GGG GCC
F V G G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
L A A A R G G R V H R A P E P Y K A
CTG GCC GCC GCC AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC CCC ATG CTC CTC GCC
Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
A N L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG
E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTC GGC CAC ATG GAG GCC ACG GGG GTG
R L D V A Y L R A L S L E V A E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTC GGC CAC CTC TCC GGC GAC GAG AAC CTG ATC

R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC

N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K V R A W I E K T L E E G R R G Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG CGG GGG TAC

V E T L F G R R R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

K S V R E A A E R R M A F N M P V Q G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTC GTC CTC GAG GCC

P K E R A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

L S A K E G I D G R G G G G H H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGA GGC GGC CAT CAT CAT CAT

H H *
CAT CAT TAA

Figure 17V

Taq DNA polymerase- (PCNA) fusion protein [Fig.17-V]

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 67)

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 68)

```

      G   G   G
// GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   [X]V Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG [O]GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GAC GCC TAC GGG GGG TAC AAG GCG GGC CGC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D   L   Y   Q   L   L   L   S   D   R   I   H   V   L   H   P   E   G   Y
```

GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC
L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG
A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
A H M D D L L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
F V G G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
L A A A R G G R V H R A P E P Y K A
CTG GCC GCC AGG AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

Y L L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC

G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG CGG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

A N L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG

E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC

N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K V R A W I E K T L E E G R R R G Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

V E T L F G R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

P K E R A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CTG GCG AAG GAG GTC ATG GAG GGG

V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG


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L   S   A   K   E   G   I   D   G   R   G   G   G   G   G   H   H   H   H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGC CAT CAT CAT CAT

H   H   //
CAT CAT //

M   P   F   E   I   V   F   E   G   A   K   E   F   A   Q   L   I   D   18
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC   54

T   A   S   K   L   I   D   E   A   A   F   K   V   T   E   D   G   I   36
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA   108

S   M   R   A   M   D   P   S   R   V   V   L   I   D   L   N   L   P   54
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG   162

S   S   I   F   S   K   Y   E   V   V   E   P   E   T   I   G   V   N   72
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC   216

M   D   H   L   K   K   I   L   K   R   G   K   A   K   D   T   L   I   90
ATG GAC CAC CTA AAG AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA   270

L   K   K   G   E   E   N   F   L   E   I   T   I   Q   G   T   A   T   108
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA   324

R   T   F   R   V   P   L   I   D   V   E   E   M   E   V   D   L   P   126
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA   378

E   L   P   F   T   A   K   V   V   V   L   G   E   V   L   K   D   A   144
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT   432

V   K   D   A   S   L   V   S   D   S   I   K   F   I   A   R   E   N   162
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT   486

E   F   I   M   K   A   E   G   E   T   Q   E   V   E   I   K   L   T   180
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT   540

L   E   D   E   G   L   L   D   I   E   V   Q   E   E   T   K   S   A   198
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA   594

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Y	G	V	S	Y	L	S	D	M	V	K	G	L	G	K	A	D	E	216
TAT	GGA	GTC	AGC	TAT	CTC	TCC	GAC	ATG	GTT	AAA	GGA	CTT	GGA	AAG	GCC	GAT	GAA	648
V	T	I	K	F	G	N	E	M	P	M	Q	M	E	Y	Y	I	R	234
GTT	ACA	ATA	AAG	TTT	GGA	AAT	GAA	ATG	CCC	ATG	CAA	ATG	GAG	TAT	TAC	ATT	AGA	702
D	E	G	R	L	T	F	L	L	A	P	R	V	E	E	*			250
GAT	GAA	GGA	AGA	CTT	ACA	TTC	CTA	CTG	GCT	CCA	AGA	GTT	GAA	GAG	TGA			

Figure 17W

Pfu DNA Polymerase (WT) -(PCNA) fusion protein [Fig.17-W]

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 67)

```
//
ccctggtcct ggggccacat atatgtttctt actgccttt atgaagaatc cccagtcgc
tctaaacctgg gttatagtga caaatcttcc tcaccaccg cccaagaagg ttatttctat
caactctaca cctccccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt
taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaggcat ggaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtctct cggcaagcct attaccgtgt ggaaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gtagagaac atccagcagt
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tgtggacatc ttcgaatacag atattccatt tgcaaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagtatg cagatgaaaa
tgaaagcaaag gtgattactt ggaaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaaagcc
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gagagtgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaacctg tagagtgggt cttacttagg aaagcctacg aaagaaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac
aggtggattc gttaaagagc cagaaaaagg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctggtttt ataccaagtc tcttgggaca ttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc

gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaaagt ttggatttaa agtcctctac attgacactg atggctctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cacgtagctg ttgcaaaagaa
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aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaatccta gaaagcgat agatatcaac tttattctt
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaaccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt
ctatctgcat gcttctcttg ctcggaanng gaggattcat aacaacagta tcaacattct

```
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct
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tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct
acaatttttt ccttgtatct cctaattgtat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt ttbgaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
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ccagggtaat gttttttaagt atgaaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtag tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatgggtgtg ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtttagc tcntcccnga
aagattgaga tgttcttggg //
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA
GAA CTT CCA TTC ACT ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG GAG TAT TAC ATT AGA
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GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Figure 17X

(PCNA) - Pfu DNA Polymerase (WT) fusion protein [Fig.17-X]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 61)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA TTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG	

//

ccctggtcct ggggccacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaanaat
taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc

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tgtggacatc ttcgaatacg atattccatt tgcaagaga tacctcatcg acaaaaggcct
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tcacgaagga gaagagtttg gaaaaggccc aattataatg attagtatg cagatgaaaa
tgaaagcaag gtgattactt gaaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
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gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
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gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggaca cctttatggg atgtttcaag
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agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac
agggtggattc gttaaagagc cagaaaaagg gtgtgtggga aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct

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ccctggtttt ataccaagtc tcttgggaca ttgttagag gaaagacaaa agattaagac
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gataaaactc ttagcaaat ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaaagt ttggatttaa agtcctctac attgacactg atggctctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataaagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtgggttta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cacgtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggc ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatat acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaatccta gaaagcgat agatatcaac ttttatctt
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta

tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctacttcaa acgccttcgt tagaaatggt
ctatctgcat gcttctcttg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga ctctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttctgacgac gtagatcttt
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aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaatgttt tgtctctttt
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ccagggtaat gttttttaagt atgaaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatgggtgtg ctactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga
aagattgaga tgttcttgg // TGA

Figure 17Y

(PCNA) - PFU DNA POLYMERASE (V93 R OR E) fusion protein [Fig.17-Y]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 27)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGA AACTTTATT GGAACATCCC CAAGATXXXC CCACATTATG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCCCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540

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GTTGAGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGCAG AAAAAGCTTG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGG AACCCTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG AATACAAAAG GTGAGATGT TGAAGAAGCT 1980
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAAT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGCCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
// TGA

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Figure 17Z

PFU DNA POLYMERASE (V93 R OR E) -(PCNA) fusion protein [Fig.17-Z]

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGAA AAGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTTGA AAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGA AGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAA AGCCTGGGA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTA AGTGGTTCTT ACTTAGGAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGAGTA TCAAAGAAG 1140
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGGT GTGGGAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAAGTCCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAAG GGTATGCAGT AATAGATGAA 1800

GAAGGAAAAG	TCATTACTCG	TGTTTAGAG	ATAGTTAGGA	GAGATTGGAG	TGAAATTGCA	1860	
AAAGAAACTC	AAGCTAGAGT	TTTGGAGACA	ATACTAAAAC	ACGGAGATGT	TGAAGAAGCT	1920	
GTGAGAAATAG	TAAAGAAGT	AATACAAAAG	CTTGCCAATT	ATGAAATTCC	ACCAGAGAAG	1980	
CTCGCAATAT	ATGAGCAGAT	AACAAGACCA	TTACATGAGT	ATAAGGCGAT	AGGTCCTCAC	2040	
GTAGCTGTTG	CAAAAGAACT	AGCTGCTAAA	GGAGTTAAA	TAAAGCCAGG	AATGTTAATT	2100	
GGATACATAG	TACTTAGAGG	CGATGGTCCA	ATTAGCAATA	GGCAATTCT	AGCTGAGGAA	2160	
TACGATCCCA	AAAAGCACAA	GTATGACGCA	GAATATTACA	TGGAGAACCA	GGTCTTCCA	2220	
GCGGTACTTA	GGATATTGGA	GGGATTGGA	TACAGAAAAG	AAGACCTCAG	ATACCAAAAG	2280	
ACAAGACAAG	TCGGCCTAAC	TTCCTGGCTT	AACATTAAA	AATCC //		2328	
ATG CCA	TTT GAA	ATC GTA	TTT GAA	GGT GCA	AAA GAG	TTT GCC CAA CTT ATA GAC	54
ACC GCA	AGT AAG	TTA ATA	GAT GAG	GCC GCG	TTT AAA	GTT ACA GAA GAT GGG ATA	108
AGC ATG	AGG GCC	ATG GAT	CCA AGT	AGA GTT	GTC CTG	ATT GAC CTA AAT CTC CCG	162
TCA AGC	ATA TTT	AGC AAA	TAT GAA	GTT GAA	CCA CCA	GAA ACA ATT GGA GTT AAC	216
ATG GAC	CAC CTA	AAG AAG	ATC CTA	AAG AGA	GGT AAA	GCA AAG GAC ACC TTA ATA	270
CTC AAG	AAA GGA	GAG GAA	AAC AAC	TTC TTA	GAG ATA	ACA ATT CAA ACT GCA ACA	324
AGA ACA	TTT AGA	GTT CCC	CTA ATA	GAT GTA	GAA GAG	ATG GAA GTT GAC CTC CCA	378
GAA CTT	CCA TTC	ACT GCA	AAG GAA	GTT GTA	GTT GGA	GAA GTC CTA AAA GAT GCT	432
GTT AAA	GAT GCC	TCT CTA	GTG AGT	GAC AGC	ATA AAA	TTT ATT GCC AGG GAA AAT	486
GAA TTT	ATA ATG	AAG GCA	GAG GGA	ACC CAG	GAA GAA	GTT GAG ATA AAG CTA ACT	540
CTT GAA	GAT GAG	GGA TTA	TTG GAC	ATC GAG	GTT CAA	GAG ACA AAG AGC GCA	594
TAT GGA	GTC AGC	TAT CTC	TCC GAC	ATG GTT	AAA GGA	CTT GGA AAG GCC GAT GAA	648
GTT ACA	ATA AAG	TTT GGA	AAT GAA	ATG CCC	ATG CAA	ATG GAG TAT TAC ATT AGA	702
GAT GAA	GGA AGA	CTT ACA	TTC CTA	CTG GCT	CCA AGA	GTT GAA GAG TGA	

Figure 17AA

PFU DNA POLYMERASE (G387P/V93R OR E) -(PCNA) fusion protein [Fig.17-AA]

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 67)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
 AAAGAGAACG GAAAATTATA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120

CTTCTCAGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGAT~~XXC~~ CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAAGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAA~~ACTTGG~~ GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAA~~TTCC~~T TCCAATGGAA ATTCA~~GCTTT~~ CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTG~~TAG~~ AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATT~~CGTT~~ AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTC~~TT~~ TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTG~~CCTG~~ GGAAGA~~AAAG~~ 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATICA AAGCTCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGA~~AA~~TTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGCGGAT AGGTCC~~T~~CAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAAT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGC~~AA~~TTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCA~~AAAG~~ 2280
ACAAGACAAG TCGGCCTAAC TTCC~~TGGCTT~~ AACATTA~~AAA~~ AATCC // 2328

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// ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

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Figure 17BR

(PCNA) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein [Fig.17-BB]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 29)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 30)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432

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GTT AAA GAT GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCCTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTTGGA AAACATAGA TCTTCCATAC 540
GTTGAGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCTC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AGCACACAGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAC AGCCAAAGT AAGAGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAAGTCCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860

AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAAATAG TAAAGAAGT AATACAAAAG CTTGCCAAATT ATGAAATTCC ACCAGAGAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
 GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGCCAATTCT AGCTGAGGAA 2160
 TAGGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAA AATCC //TAG 2328

Figure 17CC

(PCNA) -PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein [Fig.17-CC]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCITC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGCAG AAAA^{ACT}TGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGCGTGA GAAGTCAAGG GAAGAATACA TTTTCGACTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG AAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTC^{AA}GGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAGAAGG 1140
CTCAGGGAGA GCTACACA[CC N]GTT GGATTTCGTT AAAGAGCCAG AAAAGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTC^{TT}CGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAA 1980
CTCGCAATAT ATGAGCAGAT AACAAAGCCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGC^{AA}TTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220

GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

TGA

Figure 17DD

PFU DNA POLYMERASE(D141A/E143A/V93R OR E) - (PCNA) fusion protein
[Fig.17-DD]

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 67)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGAAAGAA AGCTAAAGAT TCTTGCCCTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTTAGCG 660
AAAAGGCAG AAAAAGCTTG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAAATACA TTTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTCAAGGTC AAGCACAGGG AACCTTGTA AGTGGTTCTT ACTTAGGAAA 1080

GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAGAAGG 1140
CTCAGGGGAGA GCTACACA[CC N]GTT GGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTTCT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCGTG GGAAGAAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAAG 1680
GCTCTAGAAT TTGTAAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAGG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Figure 17EE

KOD DNA POLYMERASE - (PCNA) fusion protein [Fig.17-EE]

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCCTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCCTTCG CCAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAAC TTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTACAGAGGA TGGCGACAG GTTTGCCGTC GAAGTGAAG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900
ACCGCGGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC CCTGATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTA CTGCAA GGAGTGTGCA GAGAGCGTAA CGCCTGGGG AAGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AGTACGGCT TTAAGGTAAT CTACAGCGAC 1620

ACCGACGGAT TTTTGTCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCTGCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAAGTACG AGTTCCGCC AGAGAAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTGCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Figure 17FF

(PCNA) - KOD DNA POLYMERASE fusion protein [Fig.17-FF]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC      54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA      108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG      162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC      216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA      270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA      324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA      378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT      432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT      486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT      540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA      594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA      648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA      702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //
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//ATGATCCTCG AACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTCAAG 60
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CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAAG AGTTCCTCGG GAGACCAGTT 240
GAGGTCGTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGATTAGT GCCAATGGAA GCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGA AGAACGTGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGACAAC TCGACTTCGC CTATCTGAAA 660
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TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCCTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCCTGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCGGGGC CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGC GGAGAAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17GG

(PCNA) -Vent DNA POLYMERASE FUSION PROTEIN [Fig.17-GG]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC      54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA      108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG      162
TCA AGC ATA TTT AGC AAA TAT GAA GGT GTT GAA CCA GAA ACA ATT GGA GTT AAC      216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA      270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA      324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA      378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT      432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT      486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT      540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA      594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA      648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA      702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //
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CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGCACAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGAAA AGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTGCGCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTACAAT GGGGACAATT TTGATTGCCC GTATCTCATA 660
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GATCTTTCC CAGTTGTGG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAAGCAG TTTTAGGAAA AACCAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGAAACAG AAGAAAGCAT GAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGAT GGGACGTC C GAGATCAAGC ACCGCAACC TCGTGGAGTG GTATCTTTA 1080
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CGGCGCTTAA GAACAACCTTA CCTGGAGGA TATGTAAAAG AGCCAGAAA AGGTTTGTGG 1200
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GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAA AAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
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GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAAGAG GCAGGATAAC AACAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGTTTGA GAGGCTATAC TTAAAAGAGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCC CGATAGCAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGT AATTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTGGAATACA GAAAGGAGGA TTAAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 17HH

Vent DNA POLYMERASE - (PCNA) FUSION PROTEIN [Fig.17-HH]

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACTGATTa CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAg 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGTGAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGCACAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGCT CCTTGCCCTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620

TATGCGGACA CTGACGGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA 1680
AAGAAAAGCCA AGGAATTCCCT AAACCTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTAA GAGGCTATAC TTAAAAGAGGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCTACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTCGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Figure 17II

Deep Vent- (PCNA) DNA polymerase fusion protein [Fig.17-II]

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG	ACGCTGACTA	CATCACCGAG	GATGGGAAGC	CGATTATAAG	GATTTCAAG	60
AAAGAAAACG	GCGAGTTTAA	GGTTGAGTAC	GACAGAAACT	TTAGACCTTA	CATTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAAACGCCGA	GAGGCATGGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTCCTGGG	GAGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCCT	CAGGACXXXC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTTCG	GAAAGAGGTAC	360
CTAATAGACA	AAGGCCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGACCGGTAG	TGAGCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAAGG	GACTGGAGAG	AGTTGCAAA	TATTCAATGG	AGGATGCAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCCG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500

GCAAAAGCCC GTTGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCCTG GGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GAAAGTTTCG GGTTCAAAGT CTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCCT GGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCCAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG 1800
GAAGGGAAGA TAATCACTAG GGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGCAACGT TGAGGAGGCA 1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG 1980
CTAGTTATTT ACGAGCAGAT CACGAGGCC CTTACGAGT ACAAGGCTAT AGGTCCGCAC 2040
GTTGCCGTGG CAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCCTGG CATGGTGATA 2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG // 2328

// ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GGT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAG ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Figure 17JJ

(PCNA) - Deep Vent DNA polymerase fusion protein [Fig.17-JJ]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC      54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA      108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG      162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC      216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA      270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA      324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA      378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT      432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT      486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT      540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA      594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA      648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA      702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //
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//ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTC AAG      60
AAAGAAAACG GCGAGTTTAA GTTGAGTAC GACAGAAACT TTAGACCTTA CATTACGCT      120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGCATGGG      180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCTCTGGG GAGGCCGATT      240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA      300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCCG GAAGAGGTAC      360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT      420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA      480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC      540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG      600
```


AAAGATCCCG ATGTTATAAT TACCTACAAC GCGATTCTT TCGACCTTCC CTATCTAGTT 660
AAGAGGCCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCTCGAGGC AGTTTATGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG 900
ACTGGAAGG GACTGGAGAG AGTTGCAAG AGTTCAATGG AGGATGCAAA GGTAACGTAC 960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTTCAG GAGCTGTAC AGGCTGTAGG GAATACGATG TCGCCCCAGA TAACGTCTCA 1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA 1320
AAGTTCTGCA AGGACTTCCC GGGTTTATC CCAACAGCT TCTAAAGACC CAATCGAGAA GAAAGTGCTT 1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAAGTGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG CAAACAGCT ATTATGGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC TAAGGAGTGC GAAAGTTTCG GGTTCAAAGT CTTATACATA 1560
TATATAGAGT TCGTAAGGAA GAACTGGAG GAACTTCCT CACAATTCTT GGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1620
GACACAGATG GACTCTACGC CACTCTACGC TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC 1680
GCCCTAGAGT TCGTAGATTA TCGTAGAGG GTTCTTTCGTG TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGAGAGG GGTCTTTCGTG GGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1800
GAAGGGAAGA TAATCACTAG GGGCTTGAA GGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT CCTAGAGGCT AATGAAAAG CTGAGCAAAGT ACGAAATACC TCCAGAGGCA 1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG AACTGAAAAG AACTGAAAAG CTGAGCAAAGT ACGAAATACC TCCAGAGGCA 1980
CTAGTTATTT ACGAGCAGAT CACGAGGCC CACGAGGCC CACGAGGCC CACGAGGCC CACGAGGCC CACGAGGCC 2040
GTTGCCGTGG CAAAAGGTT AGCCGCTAGA AGCCGCTAGA AGCCGCTAGA AGCCGCTAGA AGCCGCTAGA AGCCGCTAGA 2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA AGACGGGCCA AGACGGGCCA AGACGGGCCA AGACGGGCCA AGACGGGCCA 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GTATGACGCT GTATGACGCT GTATGACGCT GTATGACGCT GTATGACGCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA 2328

Figure 17KK

JDF-3 - (PCNA) fusion protein [Fig.17-KK]

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGGAGTTCGAGCCCTACTTCT
ACGGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGGAGAGCAAGGTCGTTAAGGTTAAGCGCGGAGAAAGTGAAGAAAAAGTTCCCTCGG
CAGGTCTGTGGAGGTCTGGTCCCTCTACTTCACGCACCCGACGACXXXCCGGCAATCCCGACAAAATAAGGAAGCACCCCGGTTCATCGACATCTACGAGTACGACATACCC
TTCCGCAAGCGCTACCTCATAGACAAGGGCCTAATCCCAGTGGAAAGCTTAACTCATGTCCTTGAGATCGAGACGCTCTACCCAGGGAGAAAGATTGGAA
CCGGCCGATTCTGATGATAAGCTACGCCGATGAAGCGAGCGCGGTGATAACCTGGAAGAATCGCTTACGTTGAGGTTGTCTCCACCAGAGAGATGATTAA
GCGCTTCTTGAGGTCGTTAAGGAGAGGACCCGGACGTGCTGATAACATACACGGCGACAACTTCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAAGCTTGGCGTGAGCTTT
ACCTCGGAGGACGGGAGCGGAGCATACAGCGCATGGGGACAGGTTTGGCAAGCCCAAGGAGAGATAGCCACCGCTGGGAGACCGGCGAGGGCTTGAGAG
ACCTCCGACCTACACCTTGAGGCTGTATACGAGCGGTTTTCGGCAAGCCCAAGGAGAAAGGTTCTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGCCCTCTGGGACGTTTCC
GGTCGCGCTACTCGATGGAGACCGGAGGTACCTACGAGCTTGGCAGGAGTTCTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGCCCTCTGGGACGTTTCC
CGTCCAGCACCGGCAACCTCGTGAGTGGTTCCCTAAGGAAGGCTACGAGAGGAACGAACTCGCTCCAAACAGCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGGGCT
ACGCCGTGGCTACGTCAAGGAGCCGGAGCGGGACTGTGGACAATATCGTGATCTAGACTTTCGTAGTCTCTAQCCTTCAATCATAATCACCCACAACGCTCTGCCAGATAC
GCTCAACCGGAGGGGTGTAGGAGCTACGACGTTGCCCGAGGTCGTCACAAGTTCTGCAAGGACTTCCC CGCTTCATTCGAGCCCTGCTCGGAAACCTGCTGGAGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAAGAAATCTCTCGATTACAGGCAACGCGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT
ATGCCAGGGCAAGATGGTACTGCAGGGAGTGCCCGGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAGTTTCGGTTTAAAGTCCT
CTATGCAGACACAGCGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAACAGTCAAGAAAAGGCAATGGAGTTCCTTAAACTATATCAATCCAAACTGCCCGGCTTCTC
GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAGTACCGGTCATCGACGAGGGCAAGATAACACCGCGGGCTTGAGATAGTCAGGGCGG
ACTGGAGCGAGATAGCGAAGGAGACGCGAGCGAGGGTTTGGAGCGGATACCTCAGGCACGCTGACGTTGAAGAGGCCGTAGAAATTGTAGGAAAGTCAACGAAAGCTGAGCAA
GTACGAGGTTCCCGGAGAGCTGGTTATCCACGAGCAGATAACCGCGAGCTCAAGGACTACAAGCCACCGGGCCGACGTAGCCATAGCGAAGCGTTTGGCCCGCAGAGGT
GTTAAATCCGGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGCGGACAGGGCGATTCCCTTCGACGAGTTTCGACCCGACGAAGCACAAAGTACGATG
CGGACTACTACATCGAGAACGAGGTTCTGCGGCGAGTTGAGAGAAATCCTCAGGGCCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGAAGAAG//

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54

ACC GCA AGT AAG TTA ATA GAT GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GAT GAA GGT GAA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA	

Figure 17LL

(PCNA) - JDF-3 fusion protein [Fig.17-LL]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GAT GAA GGT GAA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594

TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

//ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAGCCCGTCA TCAGGTC TTCAAGAAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGGAGTTCGAG
CCCTACTTCTACGCGCTCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAAACCGGGAGAGGCACGGCAGGTCGTTAAGGTTAAGCGCGGAGAAAGGT
GAAGAAAAAGTTCCCTCGGCAGGTCTGTGGAGGTCTGGGTCCCTCTACTTCACGCACCCCGCAGGAC~~XX~~CCGGCAATCCCGACAAAAATAAGGAAGCACCCCGCGGTCA
TCGACATCTACGAGTACGACATACCCTTTCGCCAAGCGCTACCTCATAGACAAGGCCCTAATCCCGATGGAAAGTGAAGAGCTTAAACTCATGTCTCTCGAATC
GAGACGCTCTACCAAGGGAGAGAGATTTGGAACCGGGCCGATTCTGATGATAAGCTACGCCGATGAAGCGGCGCGTGATAACCTGGAAGAAGATCGACCT
TCCTTACGTTGAGTTGTCTCCACCGAGAGGAGATGATTAGCGCTTCTTGAGGTCGTTAAGGAGAGACCCGGACGTGCTGATAACATACACGGGACAACT
TCGACTTCGCCCTACCTGA AAAAGCGCTGTGAGAAAGCTTGCGGTGAGCTTTACCTCGGAGGGACGGGAGCCGGAAGATACAGCGCATGGGGACAGGTTTGCG
GTCGAGGTGAAGGCAGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCCGACCTACACCTTGAGGCTGTATACGAGCGGTTTTCGGCAA
GCCAAGGAGAAAGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGCGAGGGCTTGAGAGGTCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACG
AGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTC
CTCCTAAGGAAGCCCTACGAGAGGAACGAACTCGCTCCCAACAGCCCGACGAGGGAGCTGGCGAGGAGAAAGGGGGCTACGCGGTGGCTACGTCAAGGAGCC
GGAGCGGGACTGTGGGACAAATATCGTGATCTTAGACTTTTCGTAGTCTCTAQ~~CC~~TCAATCATAATCACCCACAACGTCCTCGCCAGATACGCTCAACCGGAGGGGT
GTAGGAGCTACGACGTTGCCCGGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCGGCTTCATTCGAGCCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAAGATA
AAGAGGAAGATGAAGCAACTCTCGACCCGCTGGAGAAAGAAATCTCCTCGATTACAGGCCAACGCG~~GCC~~ATCAAGATTCTCGCCAAACAGCTACTACGGCTACTACGGCTA
TGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGGTTACGGCATGGGGAAGGAGTACATCGAAATGGTCA TCAGAGAGCTTGAGGAAAAGTTCGGTTTTA
AAGTCCCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGA AACAGTCAAGAAAGGCAATGGAGTTCCTTAAACTATATCAATCCCAA
CTGCCCCGGCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAAGGGCTTCTTCGTCA CGAAGAAAAGTACGCGGTCA TCGACGAGGGGCAAGATAACCCACGCG
CGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGACGCGAGGTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAA
TTGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGAGCTGGTTATCCACGAGCAGATAACGCCGCGAGCTCAAGGACTACAAGGCCACCGGC
CCGCACGTAGCCATAGCGAAgCGTTTGGCCGCCAGAGGTGTTAAAATCCGGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAAGGATAGCGGACAG
GGCGATTCCCTTCGACGAGTTCGACCCGACGAAAGCACAGTACGATCGGACTACTACATCGAGAACCCAGGTTCTGCCGGCAGTTGAGAGAAATCCTCAGGGCCCTTCG
GCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGCGCGGTGGCTGA

Figure 17MM

Sac7d gene (ACCESSION No: M87569) [Fig.17-MM]

Nucleotide sequence (SEQ ID NO: 69)

Amino acid sequence (SEQ ID NO: 70)

M	V	K	K	V	K	F	K	K	Y	K	G	E	E	K	E	V	D	T	S	18
ATG	GTG	AAG	AAG	GTA	AAG	TTC	AAG	TAT	AAG	GGT	GAA	GAG	GAA	AAA	GAA	GTA	GAC	ACT	TCA	54
K	I	K	K	K	V	W	R	V	G	K	M	V	S	F	T	T	Y	D	D	36
AAG	ATA	AAG	AAG	GTT	TGG	AGA	GTA	GGC	AAA	ATG	GTG	TCC	TTT	ACC	TAT	GAC	GAC			108
N	G	K	T	G	R	G	A	V	S	E	K	D	A	P	K	E	L			54
AAT	GGT	AAG	ACA	GGT	AGA	GGA	GCT	GTA	AGC	GAG	AAA	GAT	GCT	CCA	AAA	GAA	TTA			162
L	D	M	L	A	R	A	E	R	E	K	K	*								67
TTA	GAC	ATG	TTA	GCA	AGA	GCA	GAA	AGA	GAG	AAG	AAA	TAA								201

Figure 17NN

Sac7d-Taq DNA polymerase fusion protein [Fig.17-NN]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 70) // Amino acid sequence (SEQ ID NO: 66)

M	V	K	V	K	F	K	Y	K	G	E	E	K	E	V	D	T	S			
ATG	GTG	AAG	GTA	AAG	TTC	AAG	TAT	AAG	GGT	GAA	GAG	AAA	GAA	GTA	GAC	ACT	TCA			
K	I	K	K	V	W	R	V	G	K	M	V	S	F	T	Y	D	D			
AAG	ATA	AAG	AAG	GTT	TGG	AGA	GTA	GGC	AAA	ATG	GTG	TCC	TTT	ACC	TAT	GAC	GAC			
N	G	K	T	G	R	G	A	V	S	E	K	D	A	P	K	E	L			
AAT	GGT	AAG	ACA	GGT	AGA	GGA	GCT	GTA	AGC	GAG	AAA	GAT	GCT	CCA	AAA	GAA	TTA			


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L   D   M   L   A   R   A   E   R   E   K   K   //
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

      G   G   G
// GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   G   E   P   V   Q   A   [X]V   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG [O]GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D   L   Y   Q   L   L   S   D   R   I   H   V   L   H   P   E   G   Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K

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GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
A H M D D L L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
L A A A R G G R V H R A P E P Y K A
CTG GCC GCC GCC AGG AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

A N L L W G R L E G E E R L L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG

E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

[illegible]

Figure 1700

Taq DNA polymerase- Sac7d fusion protein [Fig.17-00]

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 69)
Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 70)

```

      G   G   G
// GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   [X]V   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG [O]GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
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Marked-Up Version

Y L L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC

G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

A N L L W G R L E E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG

E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC GTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG GGC CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A A F I A E E G W L L V A L D Y

ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTC GGC CAC CTC TCC GGC GAC GAG AAC CTG ATC
R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC
G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC
N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC
I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
K V R A W I E K T L E E G R R G Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC
V E T L F G R R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
T A A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
P K E R A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CTG GCC AAG GAG GTC ATG GAG GGG
V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG ATA GGG GAG GAC TGG

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L   S   A   K   E   G   I   D   G   R   G   G   G   G   H   H   H   H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGC CAT CAT CAT

H   H   //
CAT CAT //

M   V   K   V   K   F   K   Y   K   G   E   E   K   E   V   D   T   S
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA

K   I   K   K   V   W   R   V   G   K   M   V   S   F   T   Y   D   D
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC

N   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

L   D   M   L   A   R   A   E   R   E   K   K   //   *
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA //   TAG

```

Figure 17PP

Pfu DNA Polymerase (WT) -Sac7d fusion protein [Fig.17-PP]

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 69)

```

//
ccctggtcct gggtcacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tcaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

```

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taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc
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tgatgtagag aaggttgaga aaaagtctt cggcaagcct attaccgtgt ggaaacttta
tttggaacat cccaagatg tccccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaagaga tacctcatcg acaaggcct
aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
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tgaaagcaag gtgattactt gaaaaaacat agatcttcca tacgttgagg ttgtatcaag
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tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
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taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta
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ctcgatttcc ttggttgtag tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatgggtgtg ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtttagc tcntccnga
aagattgaga tgttcttgg //

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //TGA

Figure 17QQ

Sac7d - Pfu DNA Polymerase (WT) fusion protein [Fig.17-QQ]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 61)

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
   AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
   AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
   TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //
//
ccctggtcct ggggccacat atatgttctt actgccttt atgaagaatc cccagtcgc
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caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acgaaaaatt
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tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
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cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
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tatgacgggt gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
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caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
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taacttttac agaaataact gtctcaaatt atgacaaact ttgacatttt tacttcatta
ccagggtaat gtttttaagt atgaaaatttt tcttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtag tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaa taccagacga caatgggtgtg ctactcaag cccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga
aagattgaga tgttcttgg // TGA

Figure 17RR

Sac7d - PFU DNA POLYMERASE (V93 R OR E) fusion protein [Fig.17-RR]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 27)

Nucleotide sequence (SEQ ID NO: 69) //Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGAT~~XX~~XC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTAGCG 660
AAAAGGGCAG AAAA~~AA~~CTTG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCCAAG 720
ATGCAGAGAA TAGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA TGGACAACCT 1020
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1080
TTATGGGATG TTTCAAGGTC AGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1140
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGAGATA TCAAAAGAAG 1200
CTCAGGGAGA GCTACACAGG TGGAATTCGTT AAAGAGCCAG AAAGGGGTT GTGGGAAAAAC 1260
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1320
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1380
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1440
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1500
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1560
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTA~~CT~~GCCCTG GGGAAGAAAG 1620
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1680
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1740
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1800
GAAGGGTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1860
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1920
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1980
GTGAGAAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980

CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAA AATCC //
// TGA

Figure 17SS

PFU DNA POLYMERASE (V93 R OR E) -Sac7d fusion protein [Fig.17-SS]

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAA GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGCCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA AATAAATCTC CCAACATACA CACTAGAGCG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGCG TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGGA 900
AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AGAATTCCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACACACCT 1020

TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTTCGT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATATGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGCCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGCAAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAGG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAA AATCC // 2328
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA // TGA

Figure 17TT

PFU DNA POLYMERASE (G387P/V93R OR E) -Sac7d fusion protein [Fig.17-TT]

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTAGAGAAAG AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCCAAG 720
ATGCAGAGAA TAGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCTT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAAGAAAG 1140
CTCAGGGAGA GCTACACACC NGGATTTCGTT AAAGAGCCAG AAAGGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAAGTCCCTG GGAAGAAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCCTATG CAACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGATGTCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAAATAG TAAAAGAAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040

GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCCTAAC TTCCTGGCTT AACATTAATA AATCC // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA // TGA

Figure 17UU

PFU DNA POLYMERASE (G387P/V93R OR E) -Sac7d fusion protein [Fig.17-UU]

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: **XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)**

V93E MUTANT: **XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)**

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAAG GTTGAGAAA AGTTTCTCGG CAAGCCATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGAT**XXXC** CCACTATTAG AGAAAAAGT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTGTC AAAGAGATAC 360
CTCATCGACA AAGGCCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTC 420

GATATAGAAA CCCCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTIG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA[CC N]GTTGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGTCTCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAAT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGCAAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA GAG AAG AAA // TGA

Figure 17VV

SAC7D-PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein [Fig.17-VV]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
   AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
   AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
   TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA //
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//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAA GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTI GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GCNATAGCNA CCTCTATCA CGAAGGAGAA GAGTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAA AGCCTGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
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CTCAGGAGA GCTACACA[CC N]GTTGGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTA CTGCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAG 1680
GCTCTAGAAAT TTGTAAAATA CATAAATTCA AAGTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCTGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAAATAG TAAAAGAAGT AATACAAAAG CTTGCCAAAT ATGAAATTCC ACCAGAGAAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGCAAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAA AATCC // 2328

TGA

Figure 17WW

KOD DNA POLYMERASE - Sac7d fusion protein [Fig.17-WW]

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTCG ACAC TGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTCAAG 60

AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120

CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACGGG 180

ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240

GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXC CAGCGATAAG GGACAAAGATA 300

CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGATTAGT GCCAATGGAA GCGACGAGG AGCTGAAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCCAAT CTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAAGTT TACGCTGAGG AAATAACCAAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGCCCATCAA GATCCTGGCA AACAGCTACT ACGGTACTA CGGCTATGCA 1500
AGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCCTGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAAGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACCGGCTT CTTCGTCACG AAGAAGAAGT ATCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAAGGACG GTGACGTCGA GAAAGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAAGTACG AGTTCCGCC CCAGAAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA AAG AAG AAA // TGA

Figure 17XX

Sac7d - KOD DNA POLYMERASE fusion protein [Fig.17-XX]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA //
```

```
//ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAGC CTGTCATAAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGACTT TTGAACCTTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAAG AGTTCCTCGG GAGACCAAGT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGA AGAACGTGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCACATACA CGCTTGAGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCATGAGA GGAATGAGCT GGCCCCGAAC AAGCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
```

GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCTGGG AAGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGTCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AGAAGTTAC CGAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCCG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGCACAGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACAGGT TCTCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17YY

Sac7d-Vent DNA POLYMERASE FUSION PROTEIN [Fig.17-YY]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA //

ATGATACTGG ACAC TGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCTTCATT TTCAGCCCTA TATATATGCT 120

CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACGTGTA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGCACAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGCT CCTTGCCCTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGTGGCAT ACGCGAGGAA TGAAC TTGCA CCTGGAGGA TATGTAAGA AGCCAGAAA AGGTTTGTGG 1200
CGCGCTTAA GAACAACCTTA CTTCCGAGGA TTTCCGCAGT CTGTACCCCT CAATAATAGT TACTCACAA 1260
GAAATATCA TTTATTTGGA TTTCCGGGC CTTTCCGGGC TTTATTCCTT CCATACTCGG GGACTTAATT 1380
GTATCCCCAG ATACCCTTGA AAAAGAGGC AAAAGAGGC TGTAAAGAA ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC CTTTCCGGGC TTTATTCCTT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAAGAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTA TGCCACA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
AAGAAAAGCCA AGGAATTCCT AACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAAGAG GCAGGATAAC AACAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGG AAAGGTTTTA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAATAG CAAAATACAG GGTTCCTACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GAAAGATAA GCGATAGG GTATTTACTT 2160
ACAGAAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 17ZZ

Vent DNA POLYMERASE - Sac7d FUSION PROTEIN [Fig.17-ZZ]

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACAC TGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAAC TGTA GAGTGCTCGA TGCAGTGAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGT CCTTGCCCTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGGAA AGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAAAT TTGATTGGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTG AGAGGATGGG TGATAGTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGAT GGGACGCTC GAGATCAAGC ACCGGCAACC TCGTGAGTG GTATCTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATAA 1140
CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAG AGCCAGAAA AGGTTTGTG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCCTT CAATAATAGT TACTCACAA 1260


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GTATCCCCAG ATACCCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCTT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCTT AACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTGTGTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAAGAGG AAGTGTGAA 1920
AAAAGCTGAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTGGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //
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// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
   AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
   AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
   TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA // TGA
```

Figure 17AAA

Deep Vent- Sac7d DNA polymerase fusion protein [Fig.17-AAA]

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG	ACGCTGACTA	CATCACCAG	GATGGGAAGC	CGATTATAAG	GATTTTCAAG	60
AAAGAAAACG	GCGAGTTTAA	GTTTGAGTAC	GACAGAAACT	TTAGACCTTA	CATTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTCCTGGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCT	CAGGAC XXX C	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTTCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCC GTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGACGGTAG	TGAGCCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAAGG	GACTGGAGAG	AGTTGCAAAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AAC TTGGTGG	AGTGGTACCT	CCTCAGGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCCTCA	1260
CCGATACGC	TGAACAGGGA	AGGGTG TAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGAGGGGAA	1560
TATATAGAGT	TCGTAAAGGA	GGAACTGGAG	GAAAAGTTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG	TTAAGGAGGT	AAGTGA AAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100

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GGGTACATAG TGCTGAGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

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Figure 17BBB

Sac7d - Deep Vent DNA polymerase fusion protein [Fig.17-BBB]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

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//ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCCG GAAGAGGTAC 360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600

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AAAGATCCCG ATGTTATAAT TACCTAACAC GCGATTCTT TCGACCTTCC CTATCTAGTT 660
AAGAGGCCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCTCGAGGC AGTTTATGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG 900
ACTGGAAAGG GACTGGAGAG AGTTGCCAAG TATTCAATGG AGGATGCAAA GGTAACGTAC 960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCCTCA 1260
CCGATACGC TGAACAGGGA AGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGTTTATC CCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
AGGCAAGAAA TAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAAG AGTATGCGTT GATAGATGAG 1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAAG 1980
CTAGTTATTT ACGAGCAGAT CACGAGGCC CTTACGAGT ACAAGGCTAT AGGTCCGCAC 2040
GTTGCCGTGG CAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCCTGG CATGGTGATA 2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA 2328

Figure 17CCC

JDF-3 - sac7d fusion protein [Fig.17-CCC]

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAGCCCGTCAATCAGGTCCTTCAAGAAGGAGAAACGGCGAGTTCAGGATTGAATACGACCGGAGTTCGAGCCCTACTTCT
ACGGCTCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAAACCGCGAGAGGCACGGCAGGTCGTTAAGTTAAGCGCGGAGAAAGGTGAAGAAAAAGTTCCCTCGG
CAGGTCGTGGAGGTCGTGGTCTCTACTTACGCACCCGCAGGACXXC CGCAATCCCGACAAAATAAGGAAGCACCCCGGTCAATCGACATCTACGAGTACGACATACCC
TTGCCAAGCGCTACCTCATAGACAAAGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTGGAGATCGAGACGCTCTACCAACGAGGGAGAGAGTTTGGAA
CCGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCCGCTGATAACCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAA
GCCTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTCTGATAACATAACAACGGCGACAACTTCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTT
ACCTCGGGAGGGACGGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTTCGGTCGAGGTGAAGGCGAGGTACACTTCGACCCTTTATCCAGTCAATAAGGCGCACCATAA
ACCTCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGCGAGGCGCTTGAGAG
GGTCGGCGCTACTCGATGGAGGACCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCTCTGGGACGTTTCC
CGCTCAGCACCCGGCAACCTCGTCGAGTGGTTCTCTTAAGGAAGCCTACGAGAGGAACGAACTCGCTCCCAACAAAGCCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGGCT
ACgCGGTGGCTACGTCAAGGACCGGAGCGGGGACTGTGGGACAAATATCGTGATCTAGACTTTTCGTAGTCTCTACCTTCAATCAATAATCACCCACAACGTCTCGCCAGATAC
GCTCAACCGGAGGGGTAGGAGCTACGACGTTGCCCGGAGGTCGGTCAAAAGTTCTGCAAGGACTTCCCGGCTTCATTTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGG
CAGAAAGATAAAGAGGAAGATGAAGCAACTCTCGACCCGCTGGAGAAGAAATCTCCTCGATTACAGGCAACGGCGCATCAAGATTCTCGCCAACAGCTACTACGGCTACGCGCT
ATGCCAGGCAAGATGTACTGCAAGGAGTGCGCCGAGAGCGTTACGGCATGGGAAAGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAGATTTCGGTTTTAAAGTCTT
CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACCTGCCCGCTTCTC
GAACTCGAATACGAGGGCTTCTACGTACGGGGCTTCTTCGTACGGAAGAAAAGTACGGGTCAATCGACGAGGGGCAAGATAACCAACGCCGGGCTTGAGATAGTCAAGCGCGG
ACTGGAGCGAGATAGCGAAGGACGCAAGCGAGGGTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTGAGAAATTGTCAAGGAAGTCAACCGAAAAGCTGAGCAA
GTACGAGGTTCCGCCGAGAAAGCTGGTTATCCACGAGCAGATAACGCGGAGCTCAAGGACTACAAGGCCACCGGCCAGTAGCCATAGCGAAAGCTTTGGCCGCCAGAGGT
GTTAAATCCGGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGCGCAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCAAGTACGATG
CGGACTACTACATCGAGAACCAAGTTCTGCCGGCAGTTGAGAGAAATCCTCAGGGCTTCCGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCGAGTTCGGGCTTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAG//

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA // TAG

Figure 17DDD

Sac7d - JDF-3 fusion protein [Fig.17-DDD]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA //

// ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGGAGTTCGAGCCCTACTT
CTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAGATAAACCGGAGAGCACGGTCGTTAAGGTTAAGCGCGGAGAAAGGTGAAGAAAGTTTCCTC
GGCAGGTCGTGGAGGTCGTGGTCTCTACTTCACGCCACCGCAGGACXXXCCGGCAATCCGGCACAAATAAGGAAGCACCCCGGGTCATCGACATCTACGAGTACGACATAC
CCTTCGCCAAGCGCTACCTCATAGACACAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTCGACATCGAGACGCTCTACCCAGGGAGAGAGTTGG
AACGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGCGCGGTGATAACCTGGAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGAGGAGATGATTT
AAGCGCTTCTTGAGGTCGTTAAGGAGAAGGACCCGACGTGCTGATAACATACACGGCGACAACCTCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAAGCTTGGCGTGAGCT
TTACCCCTCGGAGGACGGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTGCGGTCGAGGTAAAGGCGAGGTACACTTCGACCTTATCCAGTCATAAGCGCGACCAT
AAACCTCCCGACCTACACCCCTTGAGGCTGTATACGAGGCGGTTTTTCGGCAAGCCCAAGGAGAGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGCGAGGGCTTGAG
AGGTCGCGCTACTCGATGAGGACGCGAGGTTACCTACGAGCTTGGCAGGAGTTCTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCTCTGGGACGTTT
CCCGTCCAGCACCGGCAACCTCGTCGAGTGGTTCTCTAAGGAAGCCCTACGAGAGAACTCGCTCCCAAGCCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGG
CTACgcCGTGCTACGTCAAGGAGCCGGAGCGGGACTGTGGACAATATCGTGATCTAGACTTTCGTAGTCTCTACCTTCAATCATATAATCACCCACAACGTCTCGCCAGAT
ACGCTCAACCGGAGGGGTGTAGGAGCTACGACGTTGCCCGGAGGTCGTCGCAAGGACTTCCCGGCTTCAATTCGAGCCCTGCTCGGAAACCTGCTGGAGGAAA
GGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAACTCTCTCGATTACAGGCAACGGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGG
CTATGCCAGGGCAAGATGTTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGAAAGGAGTACATCGAAATGGTCATCAGAGAGCTTGAGGAAAGTTCGGTTTTAAAGTC
CTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTCTTTAAACTATATCAATCCCAACTGCCCGCCTTC
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CGACTGGAGCGAGATAGCGAAGGAGACGACGGCGAGGTTTTTGGAGGCGTACTCAGGCACGGTGACGTTGAAGAGGCCGTGAGAAATTGTCAGGGAAGTCAACCGAAAAGCTGAGC
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GTGTTAAATCCGGCCCGAACTGTGATAAAGCTACATCGTTCTGTGAAGGGCTCCGGAAGGATAGCGCACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGA

TGCGGACTACTACATCGAGAACCAAGGTTCTGCCCCGCAGTTGAGAGAAATCCTCAGGGCCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCCAGAAAGACGAGGCAGGTCGGGCTTGGC
GCGTGGCTGAAGCCGAAGGGGAAGAAGTGA

Figure 17EEE

Synthetic Sso7d gene [Fig.17-EEE]:

Nucleotide sequence (SEQ ID NO: 71)

Amino acid sequence (SEQ ID NO: 72)

```
A  T  V  K  F  K  Y  K  G  E  E  K  E  V  D  I  S  K
GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GAG GTA GAC ATC TCC AAG

I  K  K  V  W  R  V  G  K  M  I  S  F  T  Y  D  E  G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

G  G  K  T  G  R  G  A  V  S  E  K  D  A  P  K  E  L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

L  Q  M  L  E  K  Q  K  K
CTG CAG ATG CTG GAG AAG CAG AAA AAG
```

Figure 17FFF

Sso7d-Taq DNA polymerase fusion protein [Fig.17-FFF]

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 72) // Amino acid sequence (SEQ ID NO: 66)

```
// A  T  V  K  F  K  Y  K  G  E  E  K  E  V  D  I  S  K
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GAG GTA GAC ATC TCC AAG

I  K  K  V  W  R  V  G  K  M  I  S  F  T  Y  D  E  G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

G  G  K  T  G  R  G  A  V  S  E  K  D  A  P  K  E  L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

L  Q  M  L  E  K  Q  K  K  // G  G  G
CTG CAG ATG CTG GAG AAG CAG AAA AAG // GGC GGC GGT
```

V T S G M L L P L F E P K G R V L L V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D G H H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A [X]V Y G F A K S L L K
AGC CGG GGG GAG CCG GTG CAG GCG [O]GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V F D A K A P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L A R L E V P G Y E A D V L A S L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L L K L S W D L A K V R T D

GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
L E S P P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
L A A A R G G R V H R A P E P Y K A
CTG GCC GCC GGC AGG GGC GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
A N L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG
E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTC AGG GCC TTG TCC CTG GAG GTG GCC ACG GGG GTG
R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC CAC CCC TTC AAC CTC AAC

S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC

N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K V R A W I E K T L E E G R R R G Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

V E T L F G R R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

P K E R A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

L S A K E G I D G R G G G H H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGA GGC GGC CAT CAT CAT CAT

H H *
CAT CAT TAA

Figure 17GGG

Pfu DNA Polymerase (WT) -Sso7d fusion protein [Fig.17-GGG]

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 71)

//
ccctggtcct ggggccacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctccccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaataatt
taagatagag catgatagaa ctttttagacc atacatttac gctctttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt
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Marked-Up Version

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ttccgggagt tttgtattgc ttagccaag gtttgggatt tttgaatcct ttaactcttg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaataaact gtctcaaatt atgacaactc ttgacatttt tacttcatta
ccagggtaat gttttttaagt atgaaaattt tcttccatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtag tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaa taccagacga caatgggtgtg ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga
aagattgaga tgttcttg //
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA
```

Figure 17HHH

PFU DNA POLYMERASE (V93 R OR E) -Sso7d fusion protein [Fig.17-HHH]

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AGAATTCCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAGAGGCCAG AAAAGGGGT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAAGTCCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680

Marked-Up Version


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GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCCTAAC TTCCTGGCTT AACATTAAA AATCC 2328
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
   ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
   GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
   CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA
```

Figure 17III

PFU DNA POLYMERASE (G387P/V93R OR E) -Sso7d fusion protein [Fig.17-III]

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 71)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGGA AAGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGGCCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
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ATGCAGAGAA TAGCGGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAGAGTC AAGCACAGGG AACCTTGTAAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAAGGAGT GGGAAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAAATAG TAAAAGAAGT AATACAAAAAG CTTGCCAATT ATGAAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCCGAT AGGTCCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG 2280
ACAAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Figure 17JJJ

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) -Sso7d fusion protein [Fig.17-
JJJ]

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 71)

Marked-Up Version

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 71)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAA AGCTAAAGAT TCTTGCCCTTC 420
GCNATAGCNA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGCCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACTT 1020
TTATGGGATG TTTCAGAGTC AAGCACAGGG AACCTTGTA AGTGGTTCTT ACTTAGGAAA 1080
GCCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA[CC N]GTTGGATTCTGTT AAAGAGCCAG AAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAAG 1680
GCTCTAGAAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAAGCT 1920
GTGAGAAATAG TAAAAGAAGT AATACAAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCCGAT AGGTCCCTAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100

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GGATACATAG TACTTAGAG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TAGGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
   ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
   GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
   CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA
```

Figure 17KKK

KOD DNA POLYMERASE - Sso7d fusion protein [Fig.17-KKK]

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATCCTCG ACACTGACTA CATAACCGAG GATGAAAGC CTGTCATAAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAAG AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCTTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GCGCAGCAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGCGGAG GAGTTCGCCG AGGGCCAAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAAC TTGGA AGAACGTGGA TCTCCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGACAACCT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTTCAGAGGA TGGCGGACAG GTTTGCCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAAGTTT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
```


GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTCGA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGTCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCTGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
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GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Figure 17L.LL

Sso7d - KOD DNA POLYMERASE fusion protein [Fig.17-L.LL]

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //

//ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAAG AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGAC~~XX~~XC CAGCGATAAG GGACAAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GCCAATGGAA GAGTTCGCG TACCTTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA TGAGGGCGAG GAGTTCGCG AGGGCCCAAT CTTATGATA 480
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCG AGGGCCCAAT CTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGA AGAACGTGA TCTCCCCTAC 540
GTTGACGTG TCTCGACGGA GAGGAGATG ATAAAGCGCT TCTCCTCGTG TGTGAAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAA 720
ATTTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCACATACA CGCTTGAGGC CGTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACCTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTA CTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCCTGGG AAGGGAGTAC 1560
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ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCTGTACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTGCA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17MMM

Sso7d-Vent DNA POLYMERASE FUSION PROTEIN [Fig.17- MMM]

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //

ATGATACTGG ACACTGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCCA TAAAGGGCGA GAGACATGGA 180
AAAACGTGTA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGCCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGGAA AGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAATT TTGATTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTA CCTGGAGGA TATGTAAAAG AGCCAGAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTTGA TTTCCGCAGT CTGTACCCCT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA 1320

Marked-Up Version

GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAA T TGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGG AAAAGCCTGA ACTCATTA 1680
AAGAAAGCCA AGGAATTCCT AAAC TACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAGAGAGG AGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTGC CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTACTT 2160
ACAGAAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAGGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 17NNN

Vent DNA POLYMERASE - Sso7d FUSION PROTEIN [Fig.17-NNN]

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACAC TGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCTCATTT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAAC TGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAAATTTGAA AGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTGCGCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720

Marked-Up Version

CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTTGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAA 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TTTATTCCT CCATACTCG GGACTTAATT 1380
GGATATAGGT TCTGCAAGGA CTTTCCGGC TTTATTCCT CCATACTCG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCCGAT CGAAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGG AAAAGCCTGA ACTCATATAA 1680
AAGAAAGCCA AGGAATTCCT AAAC TACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTAA GAGGCTATAC TTAAGAGAGG AGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACCTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAAATACG ATCCTAGAAA ACACAAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Figure 17000

Deep Vent- Ssod7 DNA polymerase fusion protein [Fig.17-000]

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAGC CGATTATAAG GATTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC 360
CTAATAGACA AAGGCCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG ATGTTATAAT TACCTACAAC GCGGATTCTT TCGACCTTCC CTATCTAGTT 660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCTCGAGGC AGTTATAGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG 900
ACTGGAAAGG GACTGGAGAG AGTTGCAAG TATTCAATGG AGGATGCAAA GGTAAACGTAC 960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGCT CTGGAGGGG 1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
AGGCAAGAAA TAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GGAAGTTTCG GAAAGTTTCG GGTCAAAGT CTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCCT GGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG 1800
GAAGGGAAGA TAATCACTAG GGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860


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AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAAG 1980
CTAGTTATT ACGAGCAGAT CACGAGGCC CTTACGAGT ACAAGGCTAT AGGTCCGCAC 2040
GTTGCCGTGG CAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCCTGG CATGGTGATA 2100
GGGTACATAG TGCTGAGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGCGAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG 2328

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA
```

Figure 17PPP

Ssod7 - Deep Vent DNA polymerase fusion protein [Fig.17-PPP]

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //
```

```
ATGATACTTG ACGTGACTA CATCACCAG GATGGGAAGC CGATTATAAG GATTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
```

Marked-Up Version

AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTCCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCCGTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAGG	GACTGGAGAG	AGTTGCAAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AAC TTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCAG	GAGCCTGTAC	CCCTCGATAA	TAA TCACCCA	TAA CGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTG TAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGAGGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAAC TGGAG	GAAAAGTT CG	GGTTC AAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAA TTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTCCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGAGATAG	TTAAGGAGGT	AAC TGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17QQQ

JDF-3 - Sso7d fusion protein [Fig.17-QQQ]

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT
ACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAGATAACCGGAGAGCACGGCAGGTCGTTAAGGTTAAGCGCGGAGAAAGTGAAGAAAAGTTCCCTCGG
CAGGTCGTGGAGGTCGTGGTCCCTACTTACGCAACCGCAGGACXXXCCGGCAATCCGGACAAAATAAGGAAGCACCCCGGTCTATCGACATCTACGAGTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGCTTAAACTCATGTCTTCGACATCGAGACGCTCTACCGAGGAGAAAGAGTTTGGAA
CCGGGCCGATTCTGATGATAAGCTACGCCGATGAAGCGAGCGCGTGATAACCTGGAAGAAAGATCGACCTTACGTTGAGGTTGTCTCCACCGAGAAAGAGATGATTAA
GCGCTTCTTGAGGTCGTTAAGGAGAAAGACCCGGACGTGCTGATAACATACACGGCGACAACTTCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAAGCTTGGCGTGAGCTTT
ACCTCGGGAGGACGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTGGTCGAGGTGAAGGCAGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAA
ACCTCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGCTTGAGAG
GGTCGCGCGCTACTCGATGGAGGACCGGAGGTTACCTACGAGCTTGGCAGGAGTTCTTCCGATGGAGCCAGCTTTCAGGCTCATCGGCCAAGGCTCTGGGACGTTTCC
CGTCCAGCACCGGCAACCTCGTCAGTGGTTCCCTTAAGGAAGCCCTACGAGAGGAACGAACCTCGCTCCCAACAAGCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGGCT
ACGCCGTGGCTACGTCAAGGAGCCGGAGCGGGACTGTGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTACCTTCAATCATATAATCACCAACGCTCTCGCCAGATAC
GCTCAACCGGAGGGGTAGGAGCTACGACGTTGCCCGAGGTCCGTCACAAGTTCTGCAAGGACTTCCCGGCTTCATTCGAGCCCTGCTCGGAAACCTGCTGGAGGAAAGG
CAGAAGATAAGAGGAAGATGAAGCAACTCTCGACCCCGCTGGAGAAGAAATCTCCTCGATTACAGGCAACGCGCATCAAGAGATTCGAGAAAGTTCTGTTTAAAGTCCT
ATGCCAGGGCAAGATGGTACTGCAGGGAGTGCAGAGCGTTACGGCATGGGGAAGGAGTACATCGAAATGGTTCATCAGAGAGCTTGAGGAAAGTTCTGTTTAAAGTCCT
CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACCGTGAAACAGTCAAGAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAACTGCCCGCTTCTC
GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCAAGAAAAGTACGCGGTCAATCGACGAGGGAAGATAACCGCGGGCTTGAGATAGTCAGGCGCG
ACTGGAGCGAGATAGCGAAGGAGACGCGAGCGAGGTTTGGAGGCGATACTCAGCACGGTGACGTTGAAGAGCCGTCAGAAATTGTCAAGGAAGTCAACCGAAAGCTGAGCAA
GTACGAGGTTCCGCCGGAGAGCTGGTTATCCACGAGCAGATAACCGCGGAGCTCAAGGACTACAAGGCCACCGGCCCGCAGTAGCCATAGCGAAGcGTTTGGCCCGCAGAGGT
GTTAAATCCGGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTTCGACCCGACGAAAGCAAAAGTACGATG
CGGACTACTACATCGAGAACCAAGGTTCTGCCGGCAGTTGAGAGAAATCCTCAGGGCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCGAGTTCGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAG//

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TAG

Figure 17RRR

Sso7d - JDF-3 fusion protein [Fig.17-RRR]

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGGAGTTCGAGCCCCTACTTCT
ACCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAAGCGCGGAGAGAGGTGAAGAAAAGTTCCCTCGG
CAGGTCGTGGAGGTCCTGGTCTCTACTTCACGCACCCGACGACXXXCCGGCAATCCGGACAAAATAAGGAAGCACCCCGGTCTATCGACATCTACGAGTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTGCATCGACGTCACCGAGGGAGAAAGATTGGAA
CCGGGCCGATTCGTGATGATAAGCTACGCCGATGAAAGCGAGCGCGGTGATAACCTGGAAGAAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGAAAGAGATGATTAA
GCGCTTCTTGAGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATACACCGCGACAACCTTCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAAGCTTGCGGTGAGCTTT
ACCTTCGGAGGACGGGACCGGAGCGAAGATACAGCGCATGGGGACAGGTTTTCGGTCGAGGTGAAGGCGAGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAA
ACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAAGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGCGGAGGGCTTGAGAG
GGTCGCGCTACTCGATGGAGACCGGAGGTTACCTACGAGCTTGGCAGGGAGTCTTCCGATGGAGCCAGCTTTCAGGCTCATCGGCCAAGCCTCTGGGACGTTTCC
CGTCCAGCACCGGCAACCTCGTCGAGTGGTTCCTCTAAGGAAGCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCCGACGAGGGAGCTGGCGAGGAAAGGGGGGCT
ACGCCGTGGCTACGTCAAGGAGCCGGAGCGGGACTGTGGGACAATATCGTGATCTAGACTTTTCGTAGTCTCTAQCCTTCAATCAATAATCACCCACAACGTCTCGCCAGATAC
GCTCAACCGGAGGGGTAGGAGCTACGACGTTCGCCCGAGGTCCGTCAAGAGTTCCTCCGGCTTCATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGCAACTCTGACCCCGTGGAGAAGAACTCTCCTCGATTACAGGCAACGGGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACACGGCT
ATGCCAGGGCAAGATGGTACTGCAGGGAGTCCGCCGAGAGCGTTACGGCATGGGAAGGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAGTTCGGTTTAAAGTCCT
CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTTGAGCGGACGCTGAAACAGTCAAGAAAAGCAATGGAGTTCTTAAACTATATCAATCCCAAACCTGCCCGCCTTCTC
GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTACGAAGAAAAGTACCGCGTCAATCGACGAGGCAAGATAACCAACCGCGGCTTGAGATAGTCAGGCGCG
ACTGGAGCGAGATAGCGAAGGAGACGCGAGGGGTTTGGAGCGGATACTCAGGCACGGTGACGTTGAAGAGGCCGTGAGAAATTGTCAGGGAAAGTCAACGAAAAGCTGAGCAA
GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACCGCGGAGCTCAAGGACTACAAGGCCACCGCGCTAGCCATAGCGAAGCGTTTGGCCCGCAGAGGT
GTTAAATCCGGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAAGGATAGCGGACAGGGCGATTCCCTTCGACGAGTTCCGACCGAAGCACAAAGTACGATG
CGGACTACTACATCGAGAACCGAGTTCTGCCGGCAGTTGAGAGAACTCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTTCGCTACCGAAGACGAGGACGAGTCTGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAAGTGA

2

[illegible]

2

[illegible]

FIGURE 18 (cited from Belova et al. (2001) Proc. Natl. Acad. Sci 98: 6015-6020)

FIGURE 19

[Fig. 19]

SEQ ID NO: 120 Synthetic Sso7d gene

GCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGACATCTCAA
GATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTACCTACGACGAGGG
CGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAGGACGCGCCGAAGGAGC
TGCTGCAGATGCTGGAGAAG CAGAAAAAG

SEQ ID NO: 121 The amino acid sequence of Sso7d.

ATVKFKYKGEEKEVDISKIKKVWRVVGKMISFTYDEGGGKTGRGAVSEKDAPKELLQ
MLEKQKK

SEQ ID NO: 122 The DNA sequence encoding the Sso7d-ΔTaq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA
GAGGTAGACATCTCAAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG
GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG
TGTCACTAGTCCCAAGGCCTGGAGGAGGCCCCCTGGCCCCCGCCGAAGGGGCC
TTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCT
GGCCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCT
CAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGC
CCTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTAC
CTCCTGGACCCTTCCAACACCACCCCGAGGGGGTGGCCCGGCGCTACGGCGGG
GAGTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGCTCTTCGCC
AACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAG
GTGGAGAGGCCCTTTCCGCTGTCTGGCCACATGGAGGCCACGGGGGTGCGC
CTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCC
GCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCG
GGACCAGCTGGAAAGGGTCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAA
GACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCGCTCCTGGAGGCCCTCCG
CGAGGCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCT
GAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCAGGACGGGCCG
CCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTC
CGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGC
CGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAG
ATAGAGCTCAGGGTGCTGGCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCT
TCCAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTTCGGCGTCC
CCCGGGAGGCCGTGGACCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCG
GGTCTCTACGGCATGTGCGGCCACCGCCTCTCCAGGAGCTAGCCATCCCTTA
CGAGGAGGCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGG
GCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGAC
CCTCTTCGGCCCGCCGCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGT
GCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGC
CGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGG
GGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCAAAAGA
GAGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCC
CCTGGCCGTGCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGC
CAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCATTA A

SEQ ID NO: 123 The amino acid sequence of Sso7d-ΔTaq fusion protein

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA
PKELLQMLEKQKKGGGVTSKALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAA
ARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLLDP
SNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREVERPLS
AVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERVLF
DELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLIH
PRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDYS
QIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFGV
LYGMSAHRLSQELAIPYEEAQAFIERYFQSPKVVRAWIEKTLEEGRRRGYVETLFGRR
RYVPDLEARVKS SVREAAERMAFNMPVQGTAADLMK LAMVKLFPRLEEMGARMMLL
QVHDEL VLEAPKERA EAVARLAKEVM EGVYPLAVPLEVEVGIGEDWLSAKEGIDGR
GGGGHHHHHH

SEQ ID NO: 124 The DNA sequence encoding the Sso7d-Taq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA
GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG
GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG
TGTCAGTAGTGGGATGCTGCCCCCTCTTTGAGCCCAAGGGCCGGGTCTCCTGGTG
GACGGCCACCACCTGGCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCA
GCCGGGGGGAGCCGGTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCCTCAAGG
CCCTCAAGGAGGACGGGGACGCGGTGATCGTGGTCTTTGACGCCAAGGCCCCCT
CCTTCCGCCACGAGGCCTACGGGGGGTACAAGGCGGGCCGGGCCCCACGCCAG
AGGACTTTCCCCGCAACTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCT
GGCGCGCCTCGAGGTCCCGGGGCTACGAGGCGGACGACGTCCTGGCCAGCCTGGC
CAAGAAGGCGGAAAAGGAGGGCTACGAGGTCCGCATCCTCACCGCCGACAAAG
ACCTTTACCAGCTCCTTTCCGACCGCATCCACGTCCTCCACCCCGAGGGGTACCT
CATCACCCCGGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCCGACCAGTGGGC
CGACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGG
CATCGGGGAGAAGACGGCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAG
CCCTCCTCAAGAACCTGGACCGGCTGAAGCCCCGCCATCCGGGAGAAGATCCTGG
CCCACATGGACGATCTGAAGCTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCT
GCCCCTGGAGGTGGACTTCGCCAAAAGGCGGGAGCCCCGACCGGGAGAGGCTTAG
GGCCTTTCTGGAGAGGCTTGAGTTTGGCAGCCTCCTCCACGAGTTCGGCCTTCTG
GAAAGCCCCAAGGCCTGGAGGAGGCCCCCTGGCCCCCGCCGGAAGGGGCCTTC
GTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCTGG
CCGCCGCCAGGGGGGGGCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCTCA
GGGACCTGAAGGAGGCGCGGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCCC
TGAGGGAAGGCCTTGGCCTCCCGCCCCGGCGACGACCCCATGCTCCTCGCCTACCT
CCTGGACCCTTCCAACACCACCCCCGAGGGGGTGGCCCCGGCGCTACGGCGGGGA
GTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGCTCTTCGCCAA
CCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAGGT
GGAGAGGCCCCCTTCCGCTGTCCTGGCCACATGGAGGCCACGGGGGTGCGCCT
GGACGTGGCCTATCTCAGGGCCTTGTCCTGGAGGTGGCCGAGGAGATCGCCCG
CCTCGAGGCCGAGGTCTTCCGCTGGCCGGCCACCCCTTCAACCTCAACTCCCGG
GACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAAG
ACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCGTCTTGAGGGCCCTCCGC
GAGGCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCTG
AAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCAGGACGGGGCCGCC
TCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTCCG
ATCCCAACCTCCAGA. ACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGCCG
GGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGAT
AGAGCTCAGGGTGCTGGCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTC
CAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTCCGGCGTCCCC

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CGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCGGG
GTCCTCTACGGCATGTCGGCCCAACGCCTCTCCCAGGAGCTAGCCATCCCTTACG
AGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGGGC
CTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGACCC
TCTTCGGCCGCGCGCGCTACGTGCCAGACCTAGAGGCCCCGGGTGAAGAGCGTGC
GGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCCGTCCAGGGCACCGCCGCCG
ACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGG
CCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGAGA
GGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTGATGGAGGGGGTGTATCCCC
TGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGCCA
AGGAGGGCATTGATGGCCGCGCGGAGGCGGGCATCATCATCATCATTA

SEQ ID NO: 125 The amino acid sequence of Sso7d-Taq fusion protein.

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGMISFTYDEGGGKTGRGAVSEKDA
PKELLQMLEKQKKGGGVTSGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGE
PVQAVYGFASLLKALKEDGDAVIVVFDKAPSFRHEAYGGYKAGRAPTPEDFPRQ
LALIKELVDLLGLARLEVPGYEADDVLASLAKKAEKEGYEVRILTADKDLYQLLSR
IHVLHPEGYLITPAWLWEKYGLR. PDQWADYRALTGDESDNLPGVKGIGEKTARKLL
EEWGSLEALLKNLDRLKPAIREKILAHMDDLKLSWDLAKVRTDLPLEVDFAKRREP
DRERLRAFLERLEFGSLLHEFGLLLESPKALEEAPWPPPEGAFVGVFLSRKEPMWADL
LALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLA
YLLDPSNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREV
ERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQL
ERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPL
PDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQIRJRAFI AEEGWLLVA
LDYSQIELRVL AHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTI
NFGVLYGMSAHRLSQELAIPEYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETL
FGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAAADLMKLMVKLFPRLEEMGA
RMLLQVHDELVLEAPKERA EAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKE
GIDGRGGGGHHHHHH

SEQ ID NO: 126 The DNA sequence encoding the Pfu-Sso7d fusion protein

ATGATTTTAGATGTGGATTACATAACTGAAGAAGGAAAACCTGTTATTAGGCTAT
TCAAAAAAGAGAACGGAAAATTTAAGATAGAGCATGATAGAACTTTTAGACCAT
ACATTTACGCTCTTCTCAGGGATGATTCAAAGATTGAAGAAGTTAAGAAAATAAC
GGGGGAAAGGCATGGAAAGATTGTGAGAATTGTTGATGTAGAGAAGGTTGAGAA
AAAGTTTCTCGGCAAGCCTATTACCGTGTGGAACTTTATTTGGAACATCCCCAA
GATGTTCCCACTATTAGAGAAAAAGTTAGAGAACATCCAGCAGTTGTGGACATCT
TCGAATACGATATTCCATTTGCAAAGAGATACCTCATCGACAAAGGCCTAATACC
AATGGAGGGGGGAAGAAGAGCTAAAGATTCTTGCCCTTCGATATAGAAACCCTCTA
TCACGAAGGAGAAGAGTTTGGAAAAGGCCCAATTATAATGATTAGTTATGCAGA
TGAAAATGAAGCAAAGGTGATTACTTGGAAAAACATAGATCTTCCATACGTTGA
GGTTGTATCAAGCGAGAGAGAGATGATAAAGAGATTTCTCAGGATTATCAGGGA
GAAGGATCCTGACATTATAGTTACTTATAATGGAGACTCATTTCGACTTCCCATAT
TTAGCGAAAAGGGCAGAAAACTTGGGATTAAATTAACCATTGGAAGAGATGGA
AGCGAGCCCAAGATGCAGAGAATAGGCGATATGACGGCTGTAGAAGTCAAGGG
AAGAATACATTTGCACTTGTATCATGTAATAACAAGGACAATAAATCTCCCAACA
TACACACTAGAGGCTGTATATGAAGCAATTTTTGGAAAGCCAAAGGAGAAGGTA
TACGCCGACGAGATAGCAAAAGCCTGGGAAAGTGGAGAGAACCTTGAGAGAGTT
GCCAAATACTCGATGGAAGATGCAAAGGCAACTTATGAACTCGGGAAAGAATTC
CTTCCAATGGAAATTCAGCTTTCAAGATTAGTTGGACAACCTTTATGGGATGTTT
CAAGGTCAAGCACAGGGAACCTTGTAGAGTGGTTCTTACTTAGGAAAGCCTACG
AAAGAAACGAAGTAGCTCCAAACAAGCCAAGTGAAGAGGAGTATCAAAGAAGG

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CTCAGGGAGAGCTACACAGGTGGATTTCGTTAAAGAGCCAGAAAAGGGGTTGTGG
GAAAACATAGTATACCTAGATTTTAGAGCCCTATATCCCTCGATTATAATTACCC
ACAATGTTTCTCCCGATACTCTAAATCTTGAGGGGATGCAAGAACTATGATATCGC
TCCTCAAGTAGGCCACAAGTTCTGCAAGGACATCCCTGGTTTTATACCAAGTCTC
TTGGGACATTTGTTAGAGGAAAGACAAAAGATTAAGACAAAAATGAAGGAACT
TTAGCAAATTCTTTCTACGGATATTATGGCTATGCAAAAGCAAGATGGTACTGTA
AGGAGTGTGCTGAGAGCGTTACTGCCTGGGGAAGAAAGTACATCGAGTTAGTAT
GGAAGGAGCTCGAAGAAAAGTTTGGATTTAAAGTCCTCTACATTGACACTGATG
GTCTCTATGCAACTATCCCAGGAGGAGAAAGTGAGGAAATAAAGAAAAAGGCTC
TAGAATTTGTAAAATACATAAATTCAAAGCTCCCTGGACTGCTAGAGCTTGAATA
TGAAGGGTTTTATAAGAGGGGATTCTTCGTTACGAAGAAGAGGTATGCAGTAAT
AGATGAAGAAGGAAAAGTCATTACTCGTGGTTTAGAGATAGTTAGGAGAGATTG
GAGTGAAATTGCAAAAGAACTCAAGCTAGAGTTTTGGAGACAATACTAAAACA
CGGAGATGTTGAAGAAGCTGTGAGAATAGTAAAAGAAGTAATACAAAAGCTTGC
CAATTATGAAATTCACCAGAGAAGCTCGCAATATATGAGCAGATAACAAGACC
ATTACATGAGTATAAGGCGATAGGTCCTCACGTAGCTGTTGCAAAGAACTAGCT
GCTAAAGGAGTTAAAATAAAGCCAGGAATGGTAATTGGATACATAGTACTTAGA
GGCGATGGTCCAATTAGCAATAGGGCAATTCTAGCTGAGGAATACGATCCCAA
AAGCACAAGTATGACGCAGAATATTACATTGAGAACCAGGTTCTTCCAGCGGTA
CTTAGGATATTGGAGGGATTTGGATACAGAAAGGAAGACCTCAGATACCAAAG
ACAAGACAAGTCGGCCTAACTTCTGGCTTAACATTAAAAAATCCGGTACCGGC
GGTGGCGGTGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGA
CATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTAC
GACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAGGACGCGCC
GAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGTGA

SEQ ID NO: 127 The amino acid sequence of the Pfu-Sso7d fusion protein

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTRFPYIYALLRDDSKJEEVKKITGERH
GKIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFA
KRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIIMISYADENEAKVITWKNID
LPYVEVVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGS
EPKMQRIGDMTAVEVKGRJHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEI
AKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGN
LVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESYTGGFVKEPEKGLWENIVYLD
FRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCCKDIPGFIPSLLGHLLEERQKIKTK
MKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIE
LVWKELEEKFGFKVLYIDTDGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYE
GFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEIAKETQARVLETILKHGDVEE
AVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVKIKPG
MVGIVIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKED
LRYQKTRQVGLTSWLNKKSGTGGGGATVKFKYKGEEKEVDISKIKKVWRVGKMIS
FTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK

SEQ ID NO: 128 The DNA sequence encoding the Sac7d-ΔTaq fusion protein

atgattacga attcgacggt gaaggtaaag ttcaagtata agggatgaaga gaaagaagta
gacacttcaa agataaagaa ggtttggaga gtaggcaaaa tgggtgtcctt tacctatgac
gacaatggta agacaggtag aggagctgta agcgagaaag atgctccaaa agaattatta
gacatgttag caagagcaga aagagagaag aaaggcggcg gtgtcactag cccaaggcc
ctggaggagg cccctggcc cccgccggaa ggggccttcg tgggctttgt gctttccgc
aaggagccca tgtgggccga tcttctggcc ctggccggcg ccaggggggg ccgggtccac
cgggcccccg agccttataa agccctcagg gacctgaagg aggcgcgggg gcttctcgcc
aaagacctga gcgttctggc cctgagggaa ggccttgcc tcccggccgg cgacgacccc
atgctcctcg cctacctcct ggacccttcc aacaccaccc ccgagggggg ggcccggcgc
tacggcgggg agtggacgga ggaggcgggg gagcgggccg ccctttccga gaggtcttc
gccaacctgt gggggaggct tgagggggag gagaggctcc tttggcttta ccgggaggtg

Marked Up Version

gagaggcccc tttccgctgt cctggcccac atggaggcca cgggggtgcg cctggacgtg
gcctatctca gggccttgtc cctggagggtg gccgaggaga tcgcccgcct cgaggccgag
gtcttccgcc tggccggcca ccccttcaac ctcaactccc gggaccagct ggaaagggtc
ctctttgacg agctagggct tcccgccatc ggcaagacgg agaagaccgg caagcgctcc
accagcgccg ccgtcctgga ggccctccgc gaggcccacc ccatcgtgga gaagatcctg
cagtaccggg agctcaccaa gctgaagagc acctacattg accccttgcc ggacctcatc
caccccagga cgggcgcgct ccacacccgc ttcaaccaga cggccacggc cacgggcagg
ctaagtagct ccgatcccaa cctccagaac atccccgtcc gcaccccgtc tgggcagagg
atccgccggg ccttcatcgc cgaggagggg tggctattgg tggccctgga ctatagccag
atagagctca gggtgctggc ccacctctcc ggcgacgaga acctgatccg ggtcttccag
gaggggcggg acatccacac ggagaccgcc agctggatgt tcggcgctcc ccgggagggc
gtggaccccc tgatgcgccc ggcggccaaag accatcaact tcggggtcct ctacggcatg
tcggcccacc gcctctccca ggagctagcc atcccttacg aggaggccca ggccttcatt
gagcgctact ttcaagagctt cccaaggtg cgggcctgga ttgagaagac cctggaggag
ggcaggaggc gggggtacgt ggagaccctc ttcggccgcc gccgctacgt gccagaccta
gaggcccggg tgaagagcgt gcgggagggc gccgagcgca tggccttcaa catgcccgtc
cagggcaccc cgcgcgacct catgaagctg gctatggtga agctcttccc caggctggag
gaaatggggg ccaggatgct ccttcaggtc cacgacgagc tggtcctcga ggccccaaaa
gagagggcgg aggccgtggc ccggctggcc aaggaggtca tggagggggg gtatcccctg
gccgtgcccc tggaggtgga ggtggggata ggggaggact ggctctccgc caaggagggc
attgatggcc gcggcgagg cgggcatcat catcatcatc attaa

SEQ ID NO: 129 The amino acid sequence of the Sac7d-ΔTaq fusion protein

MITNSTVKVKFKYKGEEKEVDTSKIKKVWRVGKMVSFTYDDNGKTGRGAVSEKDA
PKELLDMLARAEREKKGGGVTSKALEEAPWPPPEGAFVGFVLSRKEPMWADLLAL
AAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLL
DPSNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREVERP
LSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERV
LFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLI
HPRTGRLHTRFNQTATATGRLSSSDPNLQNPVRTPLGQRIRRAFIAEEGWLLVALDY
SQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFG
VLYGMSAHRLSQELAIPIYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGR
RRYVPDLEARVKS VREAAERMAFNMPVQGTAAADLMK LAMVKLFPRLEEMGARML
LQVHDELVLEAPKERA EAVARLAKEVM EGVYPLAVPLEVEVGIGEDWLSAKEGIDG
RGGGGHHHHHH

SEQ ID NO: 130 The DNA sequence encoding the PL-ΔTaq fusion protein

ATGATTACGAATTCGAAGAAAAAGAAAAAGAAAAAGCGTAAGAAACGCAAAAA
GAAAAAGAAAGGCGGCGGTGTCACTAGTGGCGCAACCGTAAAGTTCAAGTACAA
AGGCGAAGAAAAAGAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGG
GCAAGATGATCTCCTTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTG
CGGTAAGCGAAAAGGACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAG
AAAAAGGGCGGCGGTGTCAACAGTCCCAAGGCCCTGGAGGAGGCCCCCTGGCCC
CCGCCGAAGGGGCCTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGG
CCGATCTTCTGGCCCTGGCCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCG
AGCCTTATAAAGCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAG
ACCTGAGCGTTCTGGCCCTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCC
CATGCTCCTCGCCTACCTCCTGGACCCTTCCAACACCAACCCCGAGGGGGTGGCC
CGGCGCTACGGCGGGGAGTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTCC
GAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTT
TGGCTTTACCGGGAGGTGGAGAGGCCCCCTTCCGCTGTCCTGGCCACATGGAGG
CCACGGGGGTGCGCCTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGC
CGAGGAGATCGCCCGCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTC
AACCTCAACTCCCGGGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTC
CCGCCATCGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCGTCC
TGGAGGCCCTCCGCGAGGCCCAACCCATCGTGGAGAAGATCCTGCAGTACCGGG

Marked Up Version

AGCTCACCAAGCTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCC
CAGGACGGGCGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAG
GCTAAGTAGCTCCGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGG
CAGAGGATCCGCGCGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTG
GACTATAGCCAGATAGAGCTCAGGGTGCTGGCCACCTCTCCGGCGACGAGAAC
CTGATCCGGGTCTTCCAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGG
ATGTTTCGGCGTCCCCCGGGAGGCCGTGGACCCCTGATGCGCCGGGCGGCCAAG
ACCATCAACTTCGGGGTCTCTACGGCATGTGCGCCACCGCCTCTCCCAGGAGC
TAGCCATCCCTTACGAGGAGGCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTT
CCCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGG
GGTACGTGGAGACCCTCTTCGGCCGCGCCGCTACGTGCCAGACCTAGAGGCCC
GGGTGAAGAGCGTGCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCC
AGGGCACCGCCGCGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCT
GGAGGAAATGGGGGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGA
GGCCCCAAAAGAGAGGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTGATGG
AGGGGGTGTATCCCCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGG
ACTGGCTCTCCGCCAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGGCATCATC
ATCATCATCATTA

SEQ ID NO: 131 **The amino acid sequence of PL-ΔTaq fusion protein**

MITNSKKKKKKRKKRKKKKKGGGVTS GATVKFKYKGEEKEVDISKIKKVWRVGK
MISFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKKGGGVTS PKALEEAPWPPPEG
AFVGVFLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVL
ALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAAALSERLFAN
LWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLE
AEVFRLAGHPFNLNSRDQLERVLFDLGLPAIGKTEKTGKRSTSAAVLEALREAHPIV
EKILQYRELTKLKSTYIDPLPLDLPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTP
LGQRIRRAFIAEEGWLLVALDYSQIELRVLAHLSGDNLIRVFQEGRDIHTETASWMF
GVPREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPEYEAQAFIERYFQSFPKVR
AWIEKTLEEGRRRGYVETLFGRRRYVPDLEARVKS VREAAERMAFNMPVQGTAAAD
LMKLAMVKLFPRL EEMGARMLLQVHDELVLEAPKERA EAVARLAKEVM EGVYPL
AVPLEVEVGIGEDWLSAKEGIDGRGGGGHHHHHH

SEQ ID NO: 132 **PRIMER L71F 5'-CCTGCTCTGCCGCTTCACGC-3'**

SEQ ID NO: 133 **PRIMER L71R 5'-GCACAGCGGCTGGCTGAGGA-3'**

SEQ ID NO: 134 **PRIMER L18015F 15 5'-TGACGGAGGATAACGCCAGCAG-3'**

SEQ ID NO: 135 **PRIMER L23474R 5'-GAAAGACGA TGGGTCGCTAATACGC-3'**

SEQ ID NO: 136 **PRIMER L18015F 5'-TGACGGAGGATAAC GCCAGCAG-3'**

SEQ ID NO: 137 **PRIMER L29930R 5'-GGGGTTGGAGGTCAATGGGTTC-3'**

SEQ ID NO: 138 **PRIMER L3035OF 5'-CCTGCTCTGCCGCTTCACGC-3'**

SEQ ID NO: 139 **PRIMER L3512IR 30 5'- CACATGGTACAGCAAGCCTGGC-3'**

SEQ ID NO: 140 **PRIMER L2089F 5'-CCCGTATCTGCTGGGA TACTGGC-3'**

SEQ ID NO: 141 **PRIMER L7112R 5'-CAGCGGTGCTGACTGAATCATGG-3'**

SEQ ID NO: 142 **PRIMER L3035OF 5 5'-CCTGCCTGCCGCTTCACGC-3'**

Marked Up Version

SEQ ID NO: 143 **PRIMER L40547R** 5'-CCAATACCCGTTTCA TCGCGGC-3'

SEQ ID NO: 144 **PRIMER H-Amelo-Y** 5'-CCACCTCATCCTGG GCACC-3'

SEQ ID NO: 145 **PRIMER H-Amelo-YR** 5'-GCTTGAGGCCAACCATCAGAGC-3'

SEQ ID NO: 146 **Human beta-globin primer 536F** 5'-GGTTGGCCAATCTACTCCCAGG-3'

SEQ ID NO: 147 **Human beta-globin primer 536R** 5'-GCTCACTCAGTGTGGCAAAG-3'

SEQ ID NO: 148 **Human beta-globin primer 1408R** 5'-GATTAGCAAAAGGGCCTAGCTTGG- 3'

MARKED UP VERSION OF AMENDED FIGURE 20

Please replace Figure 20 with the replacement Figure below, which is marked up by way of bracketing and **DOUBLE** underlining to show the changes relative to the previous version of Figure 20.

PURIFIED THERMOSTABLE PYROCOCCUS FURIOSUS DNA POLYMERASE I

AMINO ACID SEQUENCE (SEQ ID NO: 62)

Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
20 25 30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
35 40 45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65 70 75 80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
85 90 95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile

Marked-Up Version

				165					170					175			
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys		
			180					185					190				
Arg	Phe	Leu	Arg	Ile	Ile	Arg	Glu	Lys	Asp	Pro	Asp	Ile	Ile	Val	Thr		
		195					200					205					
Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Phe	Pro	Tyr	Leu	Ala	Lys	Arg	Ala	Glu		
	210					215					220						
Lys	Leu	Gly	Ile	Lys	Leu	Thr	Ile	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys		
225					230					235					240		
Met	Gln	Arg	Ile	Gly	Asp	Met	Thr	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile		
				245					250					255			
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Thr	Arg	Thr	Ile	Asn	Leu	Pro	Thr		
			260					265					270				
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu		
		275					280					285					
Lys	Val	Tyr	Ala	Asp	Glu	Ile	Ala	Lys	Ala	Trp	Glu	Ser	Gly	Glu	Asn		
	290					295					300						
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Ala	Thr	Tyr		
305					310					315					320		
Glu	Leu	Gly	Lys	Glu	Phe	Leu	Pro	Met	Glu	Ile	Gln	Leu	Ser	Arg	Leu		
				325					330					335			
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu		
			340					345					350				
Val	Glu	Trp	Phe	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Val	Ala		
		355					360					365					
Pro	Asn	Lys	Pro	Ser	Glu	Glu	Glu	Tyr	Gln	Arg	Arg	Leu	Arg	Glu	Ser		
	370					375					380						

Marked-Up Version

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385 390 395 400

Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
405 410 415

His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
420 425 430

Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
435 440 445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
450 455 460

Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
465 470 475 480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
485 490 495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
515 520 525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
530 535 540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
545 550 555 560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
565 570 575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
580 585 590

Marked-Up Version

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
595 600 605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
610 615 620

Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
625 630 635 640

Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
645 650 655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
660 665 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
675 680 685

Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
690 695 700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705 710 715 720

Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
725 730 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
740 745 750

Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
755 760 765

Trp Leu Asn Ile Lys Lys Ser
770 775

PURIFIED THERMOSTABLE PYROCOCCUS FURIOSUS DNA POLYMERASE I

NUCLEOTIDE SEQUENCE (SEQ ID NO: 61)

Marked-Up Version

ccctggtcct	gggtccacat	atatgttctt	actcgctttt	atgaagaatc	ccccagtcgc	60
tctaacctgg	gttatagtga	caaatcttcc	tccaccaccg	cccaagaagg	ttatttctat	120
caactctaca	cctcccctat	tttctctctt	atgagatttt	taagtatagt	tatagagaag	180
gttttatact	ccaaactgag	ttagtagata	tgtggggagc	ataatgattt	tagatgtgga	240
ttacataact	gaagaaggaa	aacctgttat	taggctattc	aaaaaagaga	acggaaaatt	300
taagatagag	catgatagaa	cttttagacc	atacatttac	gctcttctca	gggatgattc	360
aaagattgaa	gaagttaaga	aaataacggg	ggaaaggcat	ggaaagattg	tgagaattgt	420
tgatgtagag	aaggttgaga	aaaagtttct	cggcaagcct	attaccgtgt	ggaaacttta	480
tttggaacat	ccccagatg	ttcccactat	tagagaaaaa	gtagagaaac	atccagcagt	540
tgtggacatc	ttcgaatacg	atattccatt	tgcaaagaga	tacctcatcg	acaaaggcct	600
aataccaatg	gagggggaag	aagagctaaa	gattcttgcc	ttcgatatag	aaaccctcta	660
tcacgaagga	gaagagtttg	gaaaaggccc	aattataatg	attagttatg	cagatgaaaa	720
tgaagcaaag	gtgattactt	ggaaaaacat	agatcttcca	tacgttgagg	ttgtatcaag	780
cgagagagag	atgataaaga	gatttctcag	gattatcagg	gagaaggatc	ctgacattat	840
agttacttat	aatggagact	cattcgactt	cccatattta	gcgaaaaggg	cagaaaaact	900
tgggattaaa	ttaaccattg	gaagagatgg	aagcgagccc	aagatgcaga	gaataggcga	960
tatgacggct	gtagaagtca	agggaagaat	acatttcgac	ttgtatcatg	taataacaag	1020
gacaataaat	ctcccaacat	acacactaga	ggctgtatat	gaagcaattt	ttggaaagcc	1080
aaaggagaag	gtatacgccg	acgagatagc	aaaagcctgg	gaaagtggag	agaaccttga	1140
gagagttgcc	aaatactcga	tggaagatgc	aaaggcaact	tatgaactcg	ggaaagaatt	1200
ccttccaatg	gaaattcagc	tttcaagatt	agttggacaa	cctttatggg	atgtttcaag	1260
gtcaagcaca	gggaaccttg	tagagtgggt	cttacttagg	aaagcctacg	aaagaaacga	1320
agtagctcca	aacaagccaa	gtgaagagga	gtatcaaaga	aggctcaggg	agagctacac	1380
aggtggattc	gttaaagagc	cagaaaaggg	gttgtgggaa	aacatagtat	acctagattt	1440
tagagcccta	tatccctcga	ttataattac	ccacaatgtt	tctcccgata	ctctaaatct	1500
tgagggatgc	aagaactatg	atatcgctcc	tcaagtaggc	cacaagttct	gcaaggacat	1560

ccttggtttt	ataccaagtc	tcttgggaca	tttgtttagag	gaaagacaaa	agattaagac	1620
aaaaatgaag	gaaactcaag	atcctataga	aaaaatactc	cttgactata	gacaaaaagc	1680
gataaaaactc	ttagcaaatt	ctttctacgg	atattatggc	tatgcaaaag	caagatggta	1740
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gaaggagctc	gaagaaaagt	ttggatttaa	agtcctctac	attgacactg	atggctctcta	1860
tgcaactatc	ccaggaggag	aaagtgagga	aataaagaaa	aaggctctag	aatttgtaaa	1920
atacataaat	tcaaagctcc	ctggactgct	agagcttgaa	tatgaagggt	tttataagag	1980
gggattcttc	gttacgaaga	agaggatatgc	agtaatagat	gaagaaggaa	aagtcattac	2040
tcgtggttta	gagatagtta	ggagagattg	gagtgaatt	gcaaaagaaa	ctcaagctag	2100
agttttggag	acaataactaa	aacacggaga	tgttgaagaa	gctgtgagaa	tagtaaaaga	2160
agtaatacaa	aagcttgcca	attatgaaat	tccaccagag	aagctcgcaa	tatatgagca	2220
gataacaaga	ccattacatg	agtataaggc	gataggtcct	cacgtagctg	ttgcaaagaa	2280
actagctgct	aaaggagtta	aaataaagcc	aggaatggta	attggataca	tagtacttag	2340
aggcgatgg	ccaattagca	atagggcaat	tctagctgag	gaatacgatc	ccaaaaagca	2400
caagtatgac	gcagaatatt	acattgagaa	ccaggttctt	ccagcggtag	ttaggatatt	2460
ggagggattt	ggatacagaa	aggaagacct	cagataccaa	aagacaagac	aagtcggcct	2520
aacttcctgg	cttaacatta	aaaaatccta	gaaaagcgat	agatatcaac	ttttattctt	2580
tctaaccctt	ttctatgaaa	gaagaactga	gcaggaatta	ccagttcttc	cgttatttta	2640
tgggtaatta	aaaacccatg	ctcttgggag	aatcttcgaa	taaaatccct	aacttcaggc	2700
tttgctaagt	gaatagaata	aacaacatca	ctcacttcaa	acgccttcgt	tagaaatgg	2760
ctatctgcat	gcttctctgg	ctcggaanng	gaggattcat	aacaacagta	tcaacattct	2820
cagagaattg	agaaacatca	gaaactttga	cttctacaac	atttctaact	ttgcaactct	2880
tcaagatttt	ctaaaagaat	tttaacggcc	tcctcgtcaa	tttcgacgac	gtagatcttt	2940
tttgctccaa	gcagagccgc	tccaatggat	aacaccctg	ttcccgccacc	caagtccgct	3000
acaatttttt	ccttgtatct	cctaattgat	aagcaagcca	aaggagagta	gatgctacct	3060
ttccgggagt	tttgatttgc	tctagccaag	gtttgggatt	tttgaatcct	ttaactctgg	3120
aaagtataat	ttcaagctcc	ttcttcttca	tgacagatga	aaaattggtt	tgtctctttt	3180

taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta	3240
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc	3300
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtggt cagactttta	3360
gacactcaaa taccagacga caatggtgtg ctactcaag ccccatatgg gttgagaaaa	3420
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntccnga	3480
aagattgaga tgttcttg	3499